

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 23:11:45 ; Search time 63.6 Seconds

(without alignments)
328.331 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987

Sequence: 1 MSLINTKIKPKFKNQAFKNGE AKWKKGECATLAPSILVKGKI 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDS5/geodata/geneseq/geneseq -emb1/AA1982.DAT:*

4: /SIDS5/geodata/geneseq/geneseq -emb1/AA1983.DAT:*

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21: /SIDS5/geodata/geneseq/geneseq -emb1/AA2000.DAT:*

22: /SIDS5/geodata/geneseq/geneseq -emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
AUU34488

ID AUU34488 standard; Protein; 187 AA.
XX
AC AUU34488;

DT DT 14-FEB-2002 (first entry)

DE E. coli cellular proliferation protein #69.

KW Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

OS Escherichia coli.

XX PN WO2001170955-A2.

XX PN 2001WO-US09180.

PP 21-MAR-2001;

XX PR 21-MAR-2001;

12	370.5	37.5	271	21	AAG23833	Arabidopsis thalia
13	370.5	37.5	271	21	AAG43901	Arabidopsis thalia
14	370.5	37.5	273	21	AAG28332	Arabidopsis thalia
15	370.5	37.5	273	21	AAG45900	Arabidopsis thalia
16	351.5	35.6	266	21	AAG0191	Arabidopsis thalia
17	350.5	199	18		AAW23715	Dirofilaria immitis
18	346.5	35.1	224	21	ABB59595	Human prostate cancer
19	346.5	35.1	256	22	ABB6037	Amino acid sequence
20	343.5	34.8	219	22	ABB6036	Amino acid sequence
21	335.5	34.0	222	22	ARB20215	Novel human diagno
22	334.8	233	21	22	AB41528	Human cancer assoc
23	33.6	206	19		AAW09722	Leishmania antigen
24	328.5	33.3	220	22	ABB6843	Drosophila melanogaster
25	324.5	32.9	198	22	ABB6040	Amino acid sequence
26	324.5	32.7	199	18	AAW0793	Natural killer cell
27	322.5	32.7	271	18	AAW1592	Natural killer cell
28	322.5	32.7	271	21	AAV43399	Human natural killer cell
29	322.5	271	22	22	AMM50249	Leishmania antigen
30	322.5	32.7	271	22	ABB82478	Drosophila melanogaster
31	322.5	32.7	271	22	ABB6038	Tryptaredoxin Peroxidase
32	31.9	199	19		AAW70221	Amino acid sequence
33	307.5	31.2	263	15	AAR6754	Leishmania antigen
34	306.5	31.1	196	22	ABB5323	New flower bud induced
35	304.5	30.9	178	18	AAW09794	Drosophila melanogaster
36	299.5	30.3	242	22	ABB5947	Human natural killer cell
37	295	29.9	187	19	AAW62792	Drosophila melanogaster
38	291.5	29.9	194	19	AAW46775	Amino acid sequence
39	283	28.7	194	22	ABB53322	Drosophila melanogaster
40	283	28.7	194	22	ABB5323	Drosophila melanogaster
41	282.5	28.6	195	22	ABB67761	Amino acid sequence
42	282.5	28.6	196	22	AAU38897	Drosophila melanogaster
43	278.2	28.2	181	14	AAU39937	Tryptaredoxin Peroxidase
44	278.1	27.1	193	12	AAR1403	Amino acid sequence
45	264.5	26.8	195	21	AAB13470	M. avium av1-3 protein
						C. trachomatis LGV

DR WPI; 2001-611495/70.
DR N-PSDB; AAS52347.

XX PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX PS Example 3; Seq ID NO 10081; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC a wide variety of organic acids which are required for cell proliferation in
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

Sequence 187 AA;

Query Match 98.3%; Score 970.5; DB 22; Length 187;

Best Local Similarity 99.5%; Pred. No. 3e-104; 0; Mismatches 0; Indels 1; Gaps 1;

QY -1 MSLINRKKIKPKRNQAFKNGEFTIELERKDTRGWSVFFFFYPADENFCVCPFLGQDVAHYE 60
Db 1 msllntkkpkfknaqfkngefieltekdegrwsy-ffyypadfcvcpftelgdvhdye 59

OY 61 ELOKLGVDWVAVSTDPHRTHKAWHSSETAKIKYAMIGDPTGALTTRNFENMRDEGLAD 120
Db 60 elqkigvdavsvstdhfhthkawhssetakikyamigoptgalltnfmnredegld 119

QY 121 RATFWVDPQGIIQAIETVACIGRASDLIRKIKAQYVASHPGEVCPAKWKEGEATLAP 180
Db 120 ratfvvpdqgqiqaietvaegirdasdlirkikaqyashpgevcpkwkegeatlap 179
QY 181 SLDLVGKI 188
Db 180 sldlvgki 187

RESULT 2

AAU38121 ID AAU38121 standard; Protein: 187 AA.

AC AAU38121;

DT 14-FEB-2002 (first entry)

XX DE Salmonella typhi cellular proliferation protein #12.
XX KW Antisense; prokaryotic cellular proliferation protein;
KW antibiotic; antibacterial; drug design.

XX OS Salmonella typhi.
XX PN WO200170955-A2.

XX PD 27-SEP-2001.

XX PP 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206548P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELTRA PHARM INC
XX PI Hasebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
XX PI Yamamoto RT, Xu HH;
XX DR WPI; 2001-611495/70.
N-PSB; AAS55980.

XX PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX PS Example 3; Seq ID NO 13714; 511pp; English.

CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC a wide variety of organic acids which are required for cell proliferation in
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

Sequence 187 AA;

Query Match 97.6%; Score 963.5; DB 22; Length 187;

Best Local Similarity 97.9%; Pred. No. 2e-103; 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 MSLINRKKIKPKRNQAFKNGEFTIELERKDTRGWSVFFFFYPADENFCVCPFLGQDVAHYE 60
Db 1 msllntkkpkfknaqfkngefieltekdegrwsy-ffyypadfcvcpftelgdvhdye 59

OY 61 ELOKLGVDWVAVSTDPHRTHKAWHSSETAKIKYAMIGDPTGALTTRNFENMRDEGLAD 120
Db 60 elqkigvdavsvstdhfhthkawhssetakikyamigoptgalltnfmnredegld 119

QY 121 RATFWVDPQGIIQAIETVACIGRASDLIRKIKAQYVASHPGEVCPAKWKEGEATLAP 180
Db 120 ratfvvpdqgqiqaietvaegirdasdlirkikaqyashpgevcpkwkegeatlap 179
QY 181 SLDLVGKI 188
Db 180 sldlvgki 187

RESULT 3

AAU3822 ID AAU3822 standard; Protein: 189 AA.

AC AAU3822;

DT 14-FEB-2002 (first entry)

QY 1 MSLINTKIKPKNQAF--KNGEFIEITEKDEGRMSVFFFPADPTEVCPTELGVDVADH 58
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 Db 1 mslinkelkplftaqafdkqkfkevtdqkgsqv-vcfypadfsvcptelidlnq 59

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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 Db 60 yeelqkigvnyfsvstdthfvkhawdhdsaiskitymiqdpsqtirnfdideatgl 119

QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
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 Db 180 qpgidivgki 189

RESULT 5

AAU37159
 XX AAU37159 standard; Protein: 189 AA.

AC AAU37159;
 XX

DT 14-FEB-2002 (first entry)

DE Staphylococcus aureus cellular proliferation protein #1329.

KW Antisense; prokaryotic cellular proliferation protein;

KW antibiotic; antibacterial; drug design.

OS Staphylococcus aureus.

XX OS
 XX WO200170955-A2.

PN PN
 XX
 PD 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 27-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELIT-) ELTRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 XX Yamamoto RT, Xu HH;

DR WPI; 2001-611495/70.
 DR N-PSDB; AAS55018.

XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.

PS Example 3; Seq ID No 12752; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp://ipo.int/pub/published_pct_sequences.

XX SQ Sequence 189 AA;

Query Match 65.3%; Score 644.5; DB 22; Length 189;
 Best local Similarity 64.2%; Pred. No. 2.1e-56; Indels 3; Gaps 2;

Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

Db 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
 | |||||
 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
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 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
 | |||||
 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
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 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
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 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
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 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
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 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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 Db 60 yeelqkigvnyfsvstdthfvkhawdhdsaiskitymiqdpsqtirnfdideatgl 119

QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
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 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
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QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
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 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
 | |||||
 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 60 yeelqkigvnyfsvstdthfvkhawdhdsaiskitymiqdpsqtirnfdideatgl 119

QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
 | |||||
 Db 180 qpgidivgki 189

QY 59 YELOLKGIVYAVASDTHFKAMHSSEITAIIKYYAMIDPTGALTRFDNMREDEGL 118
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 60 yeelqkigvnyfsvstdthfvkhawdhdsaiskitymiqdpsqtirnfdideatgl 119

QY 119 ADRAFVUDPOGIQIAEVREGIGRDAASDLURKIRKAQVASHGEVCAPKWKECATL 178
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 120 aqrgtfidpdgvgaseinadgigrdastlahkikaqyvrknpgcvcapakweegaktl 179

QY 179 APSDLIVGKI 188
 | |||||
 Db 180 qpgidivgki 189

Page 5

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the essential genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pct/published_pct_sequences](http://wipo.int/pct/published_pct_sequences).

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGODAN.
 XX
 DR WPI: 1999-135784/12.
 DR N-PSDB; RAX0099.
 XX
 PT Alkyl hydroperoxide reductase gene - converts hydrogen peroxide
 PT produced by NADH oxidase Nox-1 to water
 XX
 PS Claim 1; Page 4-5; 7pp; Japanese.
 XX
 CC The present sequence represents alkyl hydroperoxide reductase from
 CC Streptococcus mutans. The alkyl hydroperoxide reductase gene can
 CC convert hydrogen peroxide formed by Nox-1 to water.
 XX
 Sequence 186 AA;

Query Match 63.4%; Score 626; DB 20; Length 186;
 Best Local Similarity 60.6%; Pred. No. 2. 9e-64;
 Matches 114; Conservative 29; Mismatches 43; Indels 2; G: C 1
 MSITNTTPKPKNDAFKNGRERTRTEKDKPGRWSVPEFRFPADTFVCPTEGLGVNHYF

XX
 AC
 XX
 DT
 XX
 DE Pseudomonas aeruginosa cellular proliferation protein #173.
 XX
 KW Antisense; prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Pseudomonas aeruginosa.
 PN WO2001070955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US00180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206148P.
 PR 26-MAY-2000; 2000US-20727P.
 PR 23-OCT-2000; 2000US-242278P.
 PR 27-NOV-2000; 2000US-25325P.
 PR 22-DEC-2000; 2000US-257331P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr
 PI Yamamoto RT, Xu HH;
 XX
 wpt - 2001-611095/70

DR N-PSDB; AAS54042.

XX New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID NO 11776; 511PP; English.

CC The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes, their use in the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC Escherichia coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

CC pneumoniae, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC programmes. The antisense nucleic acid sequence is also useful to screen

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp://wipo.int/pub/published_pct_sequences.

XX sequence 187 AA;

SQ

Query Match 61.3%; Score 605.5; DB 22; Length 187;

Best Local Similarity 58.5%; Pred. No. 6.9e-02;

Matches 110; Conservative 32; Mismatches 45; Indels 1; Gaps 1;

QY : 1 MSLINRKIKPKKNQARKNGEIEIETKDTGRWSVFFFYPADFTFCVCPPELGVDADYE 60

Db 1 mslintqvpfkvnafungkflieteeslkqkwsvlifm-paaftncpfeiedannyg 59

QY 61 ELQKLGVWDVAVSTDTHFTHKAWHSSETTAKKIYAMIGPTGALTRNFDMRREDEGLAD 120

Db 60 efqkagaeviyvttdthfshkwhtspargqkaqfpligdthqtnafgvhippeeglal 119

QY 121 RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHPGEVCPAKWKEGETLAP 180

Db 120 rgttfinvpegyktvehsneiarvdgetvirkkaaqytaahpgcavcpakwkegektlap 179

QY 181 SIDLVSGKI 188

Db |||||||

QY 180 sldlvsgki 187

RESULT 9

ID AAU34998 standard; Protein: 187 AA.

XX AAU34998;

XX 14-FEB-2002 (first entry)

XX Enterococcus faecalis cellular proliferation protein #285.

XX Antisense: prokaryotic cellular proliferation protein;

XX KW antibiotic; antibacterial; drug design.

OS Enterococcus faecalis.

XX WO200170955-A2.

XX 27-SEP-2001.

XX PF 21-MAR-2001; 2001WO-US09180.

XX PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206948P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242278P.

PR 27-NOV-2000; 2000US-25325P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

PA (ELTR-) ELTRA PHARM INC.

XX DR N-PSDB; AAS52857.

PA Hasebeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

PI XX

PR WPI; 2001-61195/70.

PT New polynucleotides for the identification and development of

PT antibiotics, comprise sequences of antisense nucleic acids -

PT Example 3; Seq ID NO 10591; 511PP; English.

CC The invention relates to antisense inhibitors of genes essential to

CC prokaryotic cellular proliferation, their use in identifying the

CC genes, their use in the discovery of novel antibiotics, the essential

CC genes themselves and the encoded proteins. The prokaryotes used are

CC Escherichia coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*

CC pneumoniae, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The

CC invention is also useful for the identification of potential new targets

CC for antibiotic development. The antisense nucleic acids can also be used

CC to identify proteins used in proliferation, to express these proteins,

CC and to obtain antibodies capable of binding to the expressed proteins.

CC The proteins can be used to screen compounds in rational drug discovery

CC programmes. The antisense nucleic acid sequence is also useful to screen

CC for homologous nucleic acids which are required for cell proliferation in

CC a wide variety of organisms. The present sequence represents an

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp://wipo.int/pub/published_pct_sequences.

XX sequence 187 AA;

SQ

Query Match 57.1%; Score 563.5; DB 22; Length 187;

Best Local Similarity 54.3%; Pred. No. 5.2e-57;

Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;

QY : 1 MSLINRKIKPKKNQARKNGEIEIETKDTGRWSVFFFYPADFTFCVCPPELGVDADYE 60

Db 1 mnlinqkqfdccdayhdgfectrvedtgkws1-fffyfadftvcpcpelgdmghehy 59

QY 61 ELQKLGVWDVAVSTDTHFTHKAWHSSETTAKKIYAMIGPTGALTRNFDMRREDEGLAD 120

Db 60 hlgelncevsysedsahywkawadet:qkikyplapngqlarffvileasmyg 119

QY 121 RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHPGEVCPAKWKEGETLAP 180

Db 120 rasfvspegeikseyindgigrnaeelvklesqfvaehgdkvcpawqpeetip 179

QY 181 SIDLVSGKI 188

Db |||||||

QY 180 sldlvsgki 187

RESULT 10

ID AAU63080

XX AAU63080 standard; Protein: 145 AA.

AC AAU63080;

XX DT 27-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein #23976.

XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.
XX
PN WO200181581-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-US12465.

XX
PR 21-APR-2000; 2000US-199047P.

XX
PR 02-JUN-2000; 2000US-20841P.

XX
PR 07-JUL-2000; 2000US-216747P.

PA (CORT-). CORIXA CORP.
XX
PT Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX
DR WPI; 2001-616774/71.

DR N-PSDB; AAS59631.

PS Example 1; SEQ ID NO 24275; 1069pp; English.

XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
the treatment, prevention and diagnosis of medical conditions caused by
CC
P. acnes. The disorders include SAPHO syndrome (synovitis), acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
nervous system, however it is particularly involved in the inflammatory
resions associated with acne vulgaris. A method for detecting the
presence or absence of P. acnes in a patient comprises contacting a
sample with a binding agent that binds to the proteins of the invention
and determining the amount of bound protein in the sample. The
polypeptides may be used as antigens in the production of antibodies
specific for P. acnes proteins. These antibodies can be used to
down-regulate expression and activity of P. acnes polypeptides and
therefore treat P. acnes infections. The antibodies may also be used as
diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 145 AA;

Query Match 55.3%; Score 546; DB 22; Length 145;
Best Local Similarity 70.0%; Pred. No. 3.8e-55; Mismatches 22; Indels 0; Gaps 0;

Matches 98; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

Score 145 AA;

RESULT 11

ID ABG14982
ID ABG14982 standard; Protein; 1873 AA.

XX
AC ABG14982;

XX
DT 18-FEB-2002 (first entry)

XX
DE Novel human diagnostic protein #14973.

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX
OS Homo sapiens.

XX
PR WO200175067-A2.

XX
PR 23-AUG-2000; 2000US-0649167.

XX
PA 11-OCT-2001.

XX
PF 30-MAR-2001; 2001WO-US08631.

XX
PR 31-MAR-2000; 2000US-0540217.

XX
PR 23-AUG-2000; 2000US-0649167.

XX
PA (HYSE-) HYSEQ INC.

XX
PT Drmanac RT, Liu C, Tang YT;

XX
DR WPI; AAS79169.

XX
PS N-PSDB; AAS59631.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits and to assess
PT biodiversity

XX
PS Claim 20; SEQ ID NO 45341; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG0377 represent novel human
CC diagnostic amino acid sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1873 AA;

Query Match 50.4%; Score 497.5; DB 22; Length 1873;
Best Local Similarity 73.0%; Pred. No. 7e-48; Mismatches 19; Indels 15; Gaps 4;

Db 6 phelgladlyneelqamgevsvstdashvkhawhadslvgkvnytmqgpnqlqtrn 65

OY 49 PTTELGVADHVRELOELQVGVAVSDTHTHKAWSSETAKIKAMIDPTGALTRN 108

OY 109 FDNMRDEGLADRATWVDPQGIGIAEVAGTEGRDASPLRKIAQVYASHGEVCP 168

Db 66 fdiveragagqadratlvdpogiqiqyeltaegigrnatelrvkvaadqiytphgvcv 125

OY 169 AKWKEGETALPSLDLVGKI 188

Db 126 akweeqdetlapsidlvgki 145

OY 76 THFTHKAWSSETAKIKAMIDPTGALTRNFDNMREDEGLADRATWVDPQGICAI 135

PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138540.	PR	09-AUG-1999;	99US-0147935.
PR	10-JUN-1999;	99US-0138847.	PR	10-AUG-1999;	99US-0148171.
PR	14-JUN-1999;	99US-0139119.	PR	11-AUG-1999;	99US-0148319.
PR	16-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	16-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	17-JUN-1999;	99US-0139492.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139455.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139456.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139457.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139458.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0150066.
PR	18-JUN-1999;	99US-0139460.	PR	23-AUG-1999;	99US-0150080.
PR	18-JUN-1999;	99US-0139461.	PR	23-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139462.	PR	25-AUG-1999;	99US-0150566.
PR	18-JUN-1999;	99US-0139463.	PR	26-AUG-1999;	99US-0150884.
PR	18-JUN-1999;	99US-0139750.	PR	01-SEP-1999;	99US-0151065.
PR	21-JUN-1999;	99US-0139817.	PR	01-SEP-1999;	99US-0151065.
PR	22-JUN-1999;	99US-0139899.	PR	31-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	07-SEP-1999;	99US-0152363.
PR	23-JUN-1999;	99US-0140354.	PR	10-SEP-1999;	99US-0152070.
PR	24-JUN-1999;	99US-0140695.	PR	13-SEP-1999;	99US-0153158.
PR	28-JUN-1999;	99US-0140833.	PR	15-SEP-1999;	99US-0154018.
PR	29-JUN-1999;	99US-0140991.	PR	24-SEP-1999;	99US-0156559.
PR	30-JUN-1999;	99US-0141287.	PR	28-SEP-1999;	99US-015658.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0156939.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0157179.
PR	02-JUN-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155339.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142893.	PR	24-SEP-1999;	99US-0156486.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156559.
PR	12-JUL-1999;	99US-0142977.	PR	16-SEP-1999;	99US-0156936.
PR	13-JUL-1999;	99US-0143562.	PR	29-SEP-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	04-OCT-1999;	99US-0157117.
PR	15-JUL-1999;	99US-0144005.	PR	05-OCT-1999;	99US-0157753.
PR	16-JUL-1999;	99US-0144085.	PR	06-OCT-1999;	99US-0157665.
PR	17-JUL-1999;	99US-0144086.	PR	07-OCT-1999;	99US-0158029.
PR	19-JUL-1999;	99US-0144334.	PR	08-OCT-1999;	99US-0158332.
PR	20-JUL-1999;	99US-0144335.	PR	12-OCT-1999;	99US-0158659.
PR	20-JUL-1999;	99US-0144335.	PR	13-OCT-1999;	99US-0159393.
PR	20-JUL-1999;	99US-0144632.	PR	04-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144884.	PR	13-OCT-1999;	99US-0159638.
PR	21-JUL-1999;	99US-0144814.	PR	13-OCT-1999;	99US-0159925.
PR	21-JUL-1999;	99US-0145086.	PR	14-OCT-1999;	99US-0159929.
PR	22-JUL-1999;	99US-0145085.	PR	14-OCT-1999;	99US-0159331.
PR	22-JUL-1999;	99US-0145087.	PR	14-OCT-1999;	99US-0159331.
PR	22-JUL-1999;	99US-014509.	PR	14-OCT-1999;	99US-0159638.
PR	22-JUL-1999;	99US-0145192.	PR	18-OCT-1999;	99US-015984.
PR	23-JUL-1999;	99US-0145145.	PR	21-OCT-1999;	99US-016041.
PR	23-JUL-1999;	99US-0145216.	PR	21-OCT-1999;	99US-0160767.
PR	23-JUL-1999;	99US-0145224.	PR	21-OCT-1999;	99US-0160778.
PR	26-JUL-1999;	99US-0145276.	PR	21-OCT-1999;	99US-0160770.
PR	27-JUL-1999;	99US-0145913.	PR	21-OCT-1999;	99US-0160814.
PR	27-JUL-1999;	99US-0145918.	PR	21-OCT-1999;	99US-0160815.
PR	27-JUL-1999;	99US-0145919.	PR	22-OCT-1999;	99US-0160980.
PR	28-JUL-1999;	99US-0145951.	PR	22-OCT-1999;	99US-0160981.
PR	02-AUG-1999;	99US-0146386.	PR	22-OCT-1999;	99US-0160989.
PR	02-AUG-1999;	99US-0146388.	PR	23-OCT-1999;	99US-0161404.
PR	02-AUG-1999;	99US-0146389.	PR	23-OCT-1999;	99US-0161405.
PR	03-AUG-1999;	99US-0147038.	PR	25-OCT-1999;	99US-0161406.
PR	04-AUG-1999;	99US-0147302.	PR	26-OCT-1999;	99US-0161359.
PR	05-AUG-1999;	99US-0147192.	PR	26-OCT-1999;	99US-0161360.
PR	06-AUG-1999;	99US-0147303.	PR	26-OCT-1999;	99US-0161361.
PR	06-AUG-1999;	99US-0147416.	PR	28-OCT-1999;	99US-0161992.
PR	06-AUG-1999;	99US-0147416.	PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.	PR	29-OCT-1999;	99US-0162142.

Query Match 37.5%; Score 370.5; DB 21; Length 271;
 Best Local Similarity 38.3%; Pred. No. 2.2e-34;
 Matches 70; Conservative 39; Mismatches 71; Index 3; Gaps 1;

Query	Match	Score	Length	DB	21:
	Best Local Similarity	37.5%	273;		
	Matches	38.3%	Pred. No.	2.3e-34;	
	70;	Conservative	39;	Mismatches	71;
				Indels	3;
				Gaps	1;
PR	04-AUG-1999; PR	99US-0147302.			
PR	05-AUG-1999; PR	99US-0147192.			
PR	05-AUG-1999; PR	99US-0147260.			
PR	06-AUG-1999; PR	99US-0147303.			
PR	06-AUG-1999; PR	99US-0147415.			
PR	09-AUG-1999; PR	99US-0147493.			
PR	09-AUG-1999; PR	99US-0147935.			
PR	10-AUG-1999; PR	99US-0148171.			
PR	11-AUG-1999; PR	99US-0148319.			
PR	12-AUG-1999; PR	99US-0148341.			
PR	12-AUG-1999; PR	99US-0148565.			
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PR	16-AUG-1999; PR	99US-0149368.			
PR	17-AUG-1999; PR	99US-0149175.			
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PR	23-AUG-1999; PR	99US-0149902.			
PR	25-AUG-1999; PR	99US-0149930.			
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PR	22-SEP-1999; PR	99US-0155139.			
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PR	24-SEP-1999; PR	99US-0155659.			
PR	28-SEP-1999; PR	99US-0156458.			
PR	29-SEP-1999; PR	99US-0156596.			
PR	04-OCT-1999; PR	99US-0157117.			
PR	05-OCT-1999; PR	99US-0157753.			
PR	06-OCT-1999; PR	99US-0157865.			
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PR	08-OCT-1999; PR	99US-0158232.			
PR	12-OCT-1999; PR	99US-0158369.			
PR	13-OCT-1999; PR	99US-0159293.			
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PR	25-OCT-1999; PR	99US-0161406.			
PR	26-OCT-1999; PR	99US-0161359.			
PR	26-OCT-1999; PR	99US-0161360.			
PR	26-OCT-1999; PR	99US-0161361.			
PR	28-OCT-1999; PR	99US-0161920.			
PR	28-OCT-1999; PR	99US-0161992.			
PR	28-OCT-1999; PR	99US-0161993.			
PR	29-OCT-1999; PR	99US-0162142.			

PR	20-MAY-1999;	99US-0135124.	PR	02-AUG-1999;	99US-0146386.
PR	21-MAY-1999;	99US-013553.	PR	02-AUG-1999;	99US-0146388.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146389.
PR	25-MAY-1999;	99US-013621.	PR	03-AUG-1999;	99US-0147038.
PR	27-MAY-1999;	99US-0136392.	PR	04-AUG-1999;	99US-0147204.
PR	28-MAY-1999;	99US-0136782.	PR	04-AUG-1999;	99US-0147302.
PR	01-JUN-1999;	99US-013722.	PR	05-AUG-1999;	99US-0147192.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147260.
PR	04-JUN-1999;	99US-0137502.	PR	06-AUG-1999;	99US-0147303.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147116.
PR	08-JUN-1999;	99US-0138094.	PR	09-AUG-1999;	99US-0147493.
PR	10-JUN-1999;	99US-0138240.	PR	09-AUG-1999;	99US-0147935.
PR	14-JUN-1999;	99US-0139119.	PR	10-AUG-1999;	99US-0148171.
PR	16-JUN-1999;	99US-0139456.	PR	11-AUG-1999;	99US-0148319.
PR	17-JUN-1999;	99US-0139452.	PR	12-AUG-1999;	99US-0148341.
PR	18-JUN-1999;	99US-0139453.	PR	13-AUG-1999;	99US-0148565.
PR	18-JUN-1999;	99US-0139459.	PR	13-AUG-1999;	99US-0148664.
PR	18-JUN-1999;	99US-0139454.	PR	16-AUG-1999;	99US-0149368.
PR	18-JUN-1999;	99US-0139460.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139462.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139463.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139750.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139763.	PR	20-AUG-1999;	99US-0149929.
PR	21-JUN-1999;	99US-0139817.	PR	23-AUG-1999;	99US-0149902.
PR	22-JUN-1999;	99US-0139899.	PR	23-AUG-1999;	99US-0149930.
PR	23-JUN-1999;	99US-0140353.	PR	25-AUG-1999;	99US-0150566.
PR	24-JUN-1999;	99US-0140554.	PR	26-AUG-1999;	99US-0150884.
PR	26-JUN-1999;	99US-0140695.	PR	27-AUG-1999;	99US-0151065.
PR	08-JUL-1999;	99US-0140823.	PR	27-AUG-1999;	99US-0151066.
PR	29-JUN-1999;	99US-0140991.	PR	27-AUG-1999;	99US-0151080.
PR	30-JUN-1999;	99US-0141287.	PR	30-AUG-1999;	99US-0149930.
PR	01-JUL-1999;	99US-0141842.	PR	31-AUG-1999;	99US-0151438.
PR	13-JUL-1999;	99US-0143342.	PR	20-SEP-1999;	99US-0151930.
PR	14-JUL-1999;	99US-0143625.	PR	22-SEP-1999;	99US-0151939.
PR	05-JUL-1999;	99US-014290.	PR	07-SEP-1999;	99US-015293.
PR	08-JUL-1999;	99US-0142803.	PR	10-SEP-1999;	99US-0153070.
PR	09-JUL-1999;	99US-0143277.	PR	13-SEP-1999;	99US-0153758.
PR	12-JUL-1999;	99US-0142977.	PR	15-SEP-1999;	99US-0154018.
PR	19-JUL-1999;	99US-014342.	PR	16-SEP-1999;	99US-0156536.
PR	19-JUL-1999;	99US-014332.	PR	20-OCT-1999;	99US-0157117.
PR	19-JUL-1999;	99US-014333.	PR	22-SEP-1999;	99US-0157479.
PR	19-JUL-1999;	99US-014433.	PR	23-SEP-1999;	99US-015786.
PR	19-JUL-1999;	99US-0144334.	PR	10-SEP-1999;	99US-0158029.
PR	19-JUL-1999;	99US-0144335.	PR	28-SEP-1999;	99US-0156458.
PR	19-JUL-1999;	99US-0144335.	PR	29-SEP-1999;	99US-0156536.
PR	20-JUL-1999;	99US-0144332.	PR	04-OCT-1999;	99US-0157117.
PR	20-JUL-1999;	99US-014433.	PR	05-OCT-1999;	99US-0157753.
PR	21-JUL-1999;	99US-0144814.	PR	06-OCT-1999;	99US-015786.
PR	21-JUL-1999;	99US-0144815.	PR	24-OCT-1999;	99US-0155659.
PR	21-JUL-1999;	99US-0145086.	PR	28-OCT-1999;	99US-0158029.
PR	21-JUL-1999;	99US-014525.	PR	12-OCT-1999;	99US-0158369.
PR	22-JUL-1999;	99US-014532.	PR	13-OCT-1999;	99US-015923.
PR	22-JUL-1999;	99US-0145884.	PR	14-OCT-1999;	99US-0159294.
PR	22-JUL-1999;	99US-014588.	PR	13-OCT-1999;	99US-0159329.
PR	23-JUL-1999;	99US-0145145.	PR	14-OCT-1999;	99US-0159330.
PR	23-JUL-1999;	99US-0145218.	PR	14-OCT-1999;	99US-0159331.
PR	23-JUL-1999;	99US-0145224.	PR	14-OCT-1999;	99US-0159637.
PR	26-JUL-1999;	99US-0145876.	PR	14-OCT-1999;	99US-0159638.
PR	27-JUL-1999;	99US-0145913.	PR	18-OCT-1999;	99US-015954.
PR	27-JUL-1999;	99US-0145918.	PR	21-OCT-1999;	99US-0160815.
PR	27-JUL-1999;	99US-0145919.	PR	21-OCT-1999;	99US-0160980.
PR	28-JUL-1999;	99US-0145951.	PR	22-OCT-1999;	99US-0160981.
PR	28-JUL-1999;	99US-0145951.	PR	22-OCT-1999;	99US-0160989.
PR	28-JUL-1999;	99US-0145951.	PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.	PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161360.	PR	26-OCT-1999;	99US-0161369.

Search completed: May 19, 2002, 01:14:12
Job time: 7347 sec

Gentz, Reiner

Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,265

FILING DATE: 06-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-467-265-15

Query Match Similarity 34.9%; Score 344.5; DB 4; Length 198; Best Local Similarity 38.7%; Pred. No. 1.7e-33; Mismatches 67; Indels 9; Gaps 5; Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

Qy 5 NTKI-KP--FKNQAFKNGEFEIIETEKDTEGRWSVFFFYPADETFVCPTELGOVADHVE 60
 | :| || | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 5 NARIGKPAFDKFATAVWDGAFKEVKLSDYKGKY-WLFLFPPLDFVFCPEIAFSNRAE 63
 Qy 61 ELQKLGVDYAVSSTDTHFTHKAWHSSET--IAKIKYAMIGDPGALTRNFDNMRDEEG 117
 | :| || | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 64 DFRKLGCVEVLGVSVSQFNHLAWINPRKEGGGLGPNIPILGDVYRLSDGYVLTDEG 123
 Qy 118 LADRATFVVPQGIIQAIETVTAEGIGRDAASDLRKIKAQYVASHPGEVCPAKNKEGEAT 177
 | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 124 IAYRGLFIDGKGVLRQITVNDLPVGSRVDEALRLVQAQTDEH-GEVCPAGWKPGSDT 182
 Qy 178 LAPSLD 183
 | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 183 IKPNVD 188

RESULT 5

US-08-467-265-16
 ; Sequence 16, Application US/08467265

; Patent No. 5985612

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Gentz, Reiner

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

ADDRESSE: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/407,891

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/467,265

FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-407-891-15

Query Match Similarity 34.9%; Score 344.5; DB 4; Length 198; Best Local Similarity 38.7%; Pred. No. 1.7e-33; Mismatches 67; Indels 9; Gaps 5; Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

Qy 5 NTKI-KP--FKNQAFKNGEFEIIETEKDTEGRWSVFFFYPADETFVCPTELGOVADHVE 60
 | :| || | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 5 NARIGKPAFDKFATAVWDGAFKEVKLSDYKGKY-WLFLFPPLDFVFCPEIAFSNRAE 63
 Qy 61 ELQKLGVDYAVSSTDTHFTHKAWHSSET--IAKIKYAMIGDPGALTRNFDNMRDEEG 117
 | :| || | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 64 DFRKLGCVEVLGVSVSQFNHLAWINPRKEGGGLGPNIPILGDVYRLSDGYVLTDEG 123
 Qy 118 LADRATFVVPQGIIQAIETVTAEGIGRDAASDLRKIKAQYVASHPGEVCPAKNKEGEAT 177
 | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 124 IAYRGLFIDGKGVLRQITVNDLPVGSRVDEALRLVQAQTDEH-GEVCPAGWKPGSDT 182
 Qy 178 LAPSLD 183
 | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
 Db 183 IKPNVD 188

RESULT 6

US-08-467-265-16

; Sequence 16, Application US/09407891

; Patent No. 6294164

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Gentz, Reiner

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLogy: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 2; Length 257;
 Best Local Similarity 38.5%; Pred. No. 1.8e-32;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Qy 11 FKNQAERKNGERIEIETKDTECRWSVFFFVPADEFVCPTELGVDADHYEELQKGVDY 70
 Db 73 FGKTAGVNGERKELSLDDFKGKVLY-LFFPLDFTFVCPCREIVAFSDKANEFHVNCEWV 131

Qy 71 AVSTDTHFTKAWHSSET--IAKIKYAMIGDPGALTNRNFDNNRDEGLADRATFVVD 127
 Db 73 FGKTAGVNGERKELSLDDFKGKVLY-LFFPLDFTFVCPCREIVAFSDKANEFHVNCEWV 131

Qy 128 POGIIQAIETTAEGIGRDAASDLRKKAQYVASYRPGEVCPAKWKEGETLAPS 181
 Db 132 AVSDSHFSHLAWINIPRKNGLGHMNITLSDTKOISRDYGVLESAGIALRGLFIID 191

Qy 192 PNGVVKHLSVNDLPVGRSVETRLVKAFOFVETH-GEVCPANNTPESPTIKPS 244
 Db 192 PNGVVKHLSVNDLPVGRSVETRLVKAFOFVETH-GEVCPANNTPESPTIKPS 244

RESULT 7
 Sequence 16, Application US/08467265
 GENERAL INFORMATION:
 PATENT NO. 6255079
 APPLICANT: Ni, Jian
 YU, Guo-Liang
 Genitz, Reiner
 Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 CARELLA, BYRN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS:<Unknown>
 TOPOLogy: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 4; Length 257;
 Best Local Similarity 38.5%; Pred. No. 1.8e-32;
 Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

Qy 11 FKNQAERKNGERIEIETKDTECRWSVFFFVPADEFVCPTELGVDADHYEELQKGVDY 70
 Db 73 FGKTAGVNGERKELSLDDFKGKVLY-LFFPLDFTFVCPCREIVAFSDKANEFHVNCEWV 131

Qy 71 AVSTDTHFTKAWHSSET--IAKIKYAMIGDPGALTNRNFDNNRDEGLADRATFVVD 127
 Db 73 FGKTAGVNGERKELSLDDFKGKVLY-LFFPLDFTFVCPCREIVAFSDKANEFHVNCEWV 131

Qy 128 POGIIQAIETTAEGIGRDAASDLRKKAQYVASYRPGEVCPAKWKEGETLAPS 181
 Db 132 AVSDSHFSHLAWINIPRKNGLGHMNITLSDTKOISRDYGVLESAGIALRGLFIID 191

Qy 192 PNGVVKHLSVNDLPVGRSVETRLVKAFOFVETH-GEVCPANNTPESPTIKPS 244
 Db 192 PNGVVKHLSVNDLPVGRSVETRLVKAFOFVETH-GEVCPANNTPESPTIKPS 244

RESULT 8
 Sequence 16, Application US/09407891
 GENERAL INFORMATION:
 PATENT NO. 6284164
 APPLICANT: Ni, Jian
 APPLICANT: YU, Guo-Liang
 APPLICANT: Genitz, Reiner
 APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 CARELLA, BYRN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

QY 56 ADHYEEQLQKGVWVAVSTDTHTKAWHSSET--IAKIYAMICDPTGALTNRFDNM 112
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 SDRADERKKLNQCVIGASVDSFHCLAWINTPKQGGLGPMNIPLSDPKRTIAQDGVL 119
 QY 113 REDEGLADRATFWVDPQGIQAIEVTAEGIQRDASDLRKIKAAQYVASHPGEVCPAKWK 172
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 KADEXISFRGLFLIDDKGILRQITNDLPVGRSVDEIRLVQAFQFTDKH-GEVCPAGWK 178
 QY 173 EGEATLAPS 183
 Db 179 PGSDTIKPDVN 189

RESULT 11
 US-09-407-891-17
 ; Sequence 17, Application US/09407891
 ; Patent No. 6294164

GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gantz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESS: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE: 06-JUN-1995
 NAME: Ferraro, Gregory D.

CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 32800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-407-891-17

Query Match 33.3%; Score 329; DB 4; Length 199;
 Best Local Similarity 35.6%; Pred. No. 1.3e-31; No. 6.7e-31;
 Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

QY 1 MSLINKI---KPFNQAFKNGERIEETKDTGGRWSVFFFVPADEFVFCPEIIF 55
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1 MSGNAKIGPAPNFKATAWMPDGQFKDISLDVKGKY-VVFFYPLDFTFVCPEIIF 59
 QY 56 ADHYEEQLQKGVWVAVSTDTHTKAWHSSET--IAKIYAMIGDPTGALTNRFDNM 112
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 SDRADERKKLNQCVIGASVDSFHCLAWINTPKQGGLGPMNIPLSDPKRTIAQDGVL 119
 QY 113 REDEGLADRATFWVDPQGIQAIEVTAEGIQRDASDLRKIKAAQYVASHPGEVCPAKWK 172
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 KADEXISFRGLFLIDDKGILRQITNDLPVGRSVDEIRLVQAFQFTDKH-GEVCPAGWK 178
 QY 173 EGEATLAPS 182
 Db 179 PGSDTIKPDVN 188

RESULT 12
 US-08-299-162A-2
 ; Sequence 2, Application US/08299162A
 ; Patent No. 5610286

GENERAL INFORMATION:
 APPLICANT: Shau, Hungyi
 TITLE OF INVENTION: Natural Killer Cell Enhancing Factor
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David J. Oldenkamp
 STREET: 2029 Century Park East, Suite 3800
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90067

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/299,162A
 FILING DATE: August 31, 1994
 CLASSIFICATION: 526

ATTORNEY/AGENT INFORMATION:
 NAME: Oldenkamp, David J
 REFERENCE/DOCKET NUMBER: 104-280
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-277-7800
 TELEFAX: 310-277-1297

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-299-162A-2

Query Match 32.7%; Score 323; DB 1; Length 199;
 Best Local Similarity 36.8%; Pred. No. 6.7e-31;
 Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;

QY 1 MSLINKI---KPFNQAFKNGERIEETKDTGGRWSVFFFVPADEFVFCPEIIF 55
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 1 MSGNAKIGPAPNFKATAWMPDGQFKDISLDVKGKY-VVFFYPLDFTFVCPEIIF 59
 QY 56 ADHYEEQLQKGVWVAVSTDTHTKAWHSSET--IAKIYAMIGDPTGALTNRFDNM 112
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 60 SDRADERKKLNQCVIGASVDSFHCLAWINTPKQGGLGPMNIPLSDPKRTIAQDGVL 119
 QY 113 REDEGLADRATFWVDPQGIQAIEVTAEGIQRDASDLRKIKAAQYVASHPGEVCPAKWK 172
 :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
 Db 120 KADEXISFRGLFLIDDKGILRQITNDLPVGRSVDEIRLVQAFQFTDKH-GEVCPAGWK 178
 QY 173 EGEATLAPS 182
 Db 179 PGSDTIKPDVN 188

RESULT 13
 US-08-467-265-14

Page 8

CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.30
DISPENSING INFORMATION: *[Redacted]*

FILING DATE:

CLASSIFICATION: PUBLIC APPLICATION DATA:

ABSTRACT NUMBER: NE 08/167 266

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION

REGISTRATION NUMBER: 36/134

REFERENCE/BUCKET NUMBER: 323800-436

TELEPHONE: 201-994-1700

TELEFAX : 201-994-1444

SEQUENCE CHARACTERISTICS:

LENGTH: 199 amino acids

STRANDEDNESS:

TOPOLOGY: Linear

407-891-14

Query Match 32.7%; Score 323; DB 4; Length 199;
 Best Jaccard Similarity 36.8%; Pred. No. 5; DB 4;
 Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;

QY		1	M\$!INT!---KPKFNOA-FKNGE\$IE\$TEKOPDEGRMSVFFYPA\$T\$FVCPIELGDY	55
		1	: : : : : : : : : : : :	
		1	MSGNAGAKIGHPA\$N\$KATAVMPD\$O\$K\$N\$LS\$DK\$KY-WF\$YPLD\$T\$FVCPEIAT	59
QY		56	ADHYEELOKLGDWYAVSTDTHKAMHSSET--IAKIKYAMIDGPTGALT\$RNFDNM	112
	:	1	: :	
		60	SDR\$AEFFK\$NLQVIGASVDSHFC\$HLAWNTPKQGGLGP\$M\$N\$PLVSDB\$RT\$IAQDGVL	119
QY		113	REDEGLADRATFVUDPQGIIQATEVTAEGIGRDA\$DL\$RR\$KIAAQYVASH\$GEVCPAKRM	172
	:	120	KADEGISFRGLFIDDKGILRQITVNDPCCRSVDET\$RLVQAFOFTDKH-GEVCPAGWK	178
		173	E\$EATL\$PL\$	182
bb		179	PASDT\$KPDV	188

Search completed: May 19, 2002, 01:15:02
Job time: 7152 sec

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On protein - protein search, using sw model				
Run on:	May 19, 2002, 00:29:30 ; Search time 51.62 Seconds			
Title:	US-09-679-705-24			
Perfect score:	987			
Sequence:	1 MSLINTKIKPKFKNQAFKNGE..... AKWKEGEATLAPSNDLVGKI 188 (without alignments) 349.957 Million cell updates/sec			
Scoring table:	BLOSUM62			
Gapop 10.0 , Gapext 0.5				
Searched:	283138 seqs, 96089334 residues			
Total number of hits satisfying chosen parameters:	283138			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries			
Database :	PIR.71: 1: pir1: 2: pir2: 3: pir3: 4: pir4: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	970.5	98.3	187	JN0289
2	970.5	98.3	187	D90709
3	970.5	98.3	187	H8559
4	963.5	97.6	187	AB0577
5	742.5	75.2	187	DB7610
6	677.5	72.3	206	GB2668
7	677.5	68.6	187	F99583
8	644.5	65.3	189	FR9804
9	624.5	63.3	168	2
10	622.5	63.1	184	A35441
11	612.5	62.1	179	S52934
12	605.5	61.3	187	C83627
13	603.5	61.1	187	A86667
14	488.5	49.5	188	D71314
15	455.5	46.1	211	D70343
16	365	37.0	242	S49173
17	362	36.7	210	T06318
18	361	36.6	198	A57716
19	354	35.9	265	2
20	34.9	34.5	198	168897
21	33.8	34.2	2	I52425
22	33.5	34.2	257	2
23	33.4	33.8	199	A67111
24	33.4	33.8	2	T56005
25	33.0	33.4	203	2
26	32.9	33.4	200	2
27	32.9	33.3	199	A48513
28	32.4	32.9	195	2
29	32.2	32.7	J02258	
2	32.7	32.7	G01790	
ALIGNMENTS				
RESULT	1			
JN0289	N; Alternative names: sulfate starvation-induced protein SSI8 C; Species: Escherichia coli C; Date: 16-Sep-1992 #sequence_revision 30-Sep-1997 #text_change 11-Jun-1999 C; Accession: C64794; JN0289; 578624 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.; Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Reference number: A64720; MUID:97426617 A; Accession: C64794 A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-187 <BLAT> A; Cross-references: GB:AE00166; GB:U00096; NID:91786819; PIDN: AAC73706.1; PID:917868 A; Experimental source: strain K-12, substrain MG1655 R; Ueshima, R.; Fujita, N.; Ishihama, A.; Biochem. Biophys. Res. Commun. 184, 634-639, 1992 A; Title: Identification of Escherichia coli proteins cross-reacting with antibodies a A; Reference number: JN0286; MUID:92246944 A; Accession: JN0289 A; Molecule type: protein A; Residues: 2-31 <UES> A; Note: this protein fragment has exact coincidence, except 1le-24, with the first 31 R; Quadroni, M.; Staudenmann, W.; Kertesz, M.; James, P.; Eur. J. Biochem. 239, 773-781, 1996 A; Title: Analysis of global responses by protein and peptide fingerprinting of protein coli. A; Reference number: S78617; MUID:96370830 A; Accession: S78624 A; Molecule type: protein A; Residues: 2-11 <QUA> A; Genetics: A; Gene: ahpc C; Superfamily: alkyl hydroperoxidase C; Keywords: oxidoreductase F; 2-187/Product: alkyl hydroperoxidase c22 protein homology <C22> F; 11-146/Domain: alkyl hydroperoxidase c22 protein homology <C22>			
Query Match	98.3%; Score 970.5; DB 2; Length 187; Best Local Similarity 99.5%; Pred. No. 3e-81; Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;			
Qy	1 MSLINTKIKPKFKNQAFKNGEFEITEKDTEGRWSVFFYPADETFVCPTELGVDHYE 60			
Db	1 MSLINTKIKPKFKNQAFKNGEFEITEKDTEGRWSVFFYPADETFVCPTELGVDHYE 59			
Qy	61 ELQLGIVDWWAVSTDTHFKAWHSSETIJKYAMGDTGALTRNFDNMREDEGLAD 120			

Qy	121	RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHGEVCPAKWKEGEATLAP	180	C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 C;Keywords: oxidoreductase
Db	120	RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHGEVCPAKWKEGEATLAP	179	
Qy	181	SLDLVGKI 188		
Db	180	SLDLVGKI 187		
RESULT 2				
D90709		alkyl hydroperoxide reductase C22 subunit [imported] - Escherichia coli (strain 0157:H7, <i>Escherichia coli</i>)		
C;Species:				
C;Date:	18-Jul-2001	#sequence_revision 18-Jul-2001 #text_change 03-Aug-2001		
C;Accession:	D90709			
R;Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.				
VIA RES. 8, 11-22, 2001				
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gene reference number: A99629; MUID:21156231; PMID:11258796				
A;Accession: D90709				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-187 <HAY>				
A;Cross-references: GB:BA00007; PIDN:BAR34067_1; PID:g13360102; GSPDB:GN00154				
A;Experimental source: strain 0157:H7, substrain RIMD 0509952				
C;Experimental source: strain 0157:H7, substrain RIMD 0509952				
C;Genetics:				
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein				
Query Match 98.3%; Score 970.5; DB 2; Length 187; Best local Similarity 99.5%; Pred. No. 3e-81; Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1; C;Accession: EC0644				
Qy	1	MSLINTKIKPKFKNAQFKNGEFEIETEKDEGRGSVFFFYPADFTFVCPTELGDVADYE 60		
Db	1	MSLINTKIKPKFKNAQFKNGEFEIETEKDEGRGSVFFFYPADFTFVCPTELGDVADYE 59		
Qy	121	RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHGEVCPAKWKEGEATLAP	180	
Db	120	RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHGEVCPAKWKEGEATLAP	179	
Qy	181	SLDLVGKI 188		
Db	180	SLDLVGKI 187		
RESULT 4				
AB0577		alkyl hydroperoxide reductase c22 protein [imported] - <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typiphila</i>		
C;Species:				
A;Note: this species has also been called <i>Salmonella typhi</i>				
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001				
C;Accession: AB0577				
R;Parry, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrington, S.; Moule, S.; O'Gaora, P.				
Nature 413, 848-852, 2001				
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.; Title: Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar <i>Typiphila</i>				
A;Reference number: AB0502; PMID:11677608				
A;Accession: AB0577				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-187 <PAR>				
A;Cross-references: GB:AL513382; PIDN:CAD05084_1; PID:g16501859; GSPDB:GN00176				
C;Genetics:				
A;Gene: SRI0653				
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein				
Query Match 97.6%; Score 963.5; DB 2; Length 187; Best local Similarity 97.9%; Pred. No. 1.3e-80; Matches 184; Conservative 3; Mismatches 0; Indels 1; Gaps 1; C;Accession: AB0559				
Qy	1	MSLINTKIKPKFKNAQFKNGEFEIETEKDEGRGSVFFFYPADFTFVCPTELGDVADYE 60		
Db	1	MSLINTKIKPKFKNAQFKNGEFEIETEKDEGRGSVFFFYPADFTFVCPTELGDVADYE 59		
Qy	61	ELQKLGVDVYAVSTDHFTKAWHSSETIARIKIAMIDGPTGALLTRNFDNMREDEGLAD 120		
Db	60	ELQKLGVDVYAVSTDHFTKAWHSSETIARIKIAMIDGPTGALLTRNFDNMREDEGLAD 119		
Qy	121	RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHGEVCPAKWKEGEATLAP	180	
Db	120	RATFVVDPOGIQIAEVTAEGIGRDAASDLRKIKAAQYVASHGEVCPAKWKEGEATLAP	179	
Qy	181	SLDLVGKI 188		
Db	180	SLDLVGKI 187		
RESULT 3				
AB0559		alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Escherichia coli (strain 0157:H7, <i>Escherichia coli</i>)		
C;Species:				
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2001				
C;Accession:	AB0559			
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Bimalalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001				
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.				
A;Reference number: A85480; MUID:21074935; PMID:11206551				
A;Accession: AB0559				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-187 <STO>				
A;Cross-references: GB:AE005174; MUID:91213501; PIDN:AAG54940_1; GSPDB:GN00145; UWGP:207				
A;Experimental source: strain 0157:H7, substrain EDL933				
C;Genetics:				
A;Gene: ahpC				

C;Species: Caulobacter crescentus	Query Match 72.3%; Score 714; DB 2; Length 206;	
C;Accession: D87610	Best Local Similarity 69.1%; Pred. No. 8; ge-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;	
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, N.J.; Emrulaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; proc. Natl. Acad. Sci. U.S.A., 98, 4135-4141, 2001	A;Title: Complete Genome Sequence of Caulobacter crescentus.	
A;Reference number: A87249; MUID:21173698; PMID:11259647	A;Accession: D87610	
A;Status: preliminary	A;Molecule type: DNA	
A;Residues: 1-187 <S>O>	C;Cross-references: GB:AE005673; NID:913424540; PIDN:AAR24880.1; GSDB:GN00148	
A;Genetics:	C;Superfamily: alky l hydroperoxide reductase c22 protein; alky l hydroperoxidase c22 p	
A;Superfamily: alky l hydroperoxide reductase c22 protein; alky l hydroperoxidase c22 prot	C;Genetics:	
Query Match 75.2%; Score 742.5; DB 2; Length 187; Best Local Similarity 72.3%; Pred. No. 2e-60; Matches 136; Conservative 27; Mismatches 24; Indels 1; Gaps 1; Matches 136; Conservative 27; Mismatches 24; Indels 1; gaps 1;	QY 1 MSЛИNTKIKРPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	
Db 1 MSЛNTEIКРРKPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	QY 1 MSЛИNTKIKРРKPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	
Db 1 MSЛNTEIКРРKPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	QY 1 MSЛИNTKIKРРKPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	
Db 61 ELOKLGVDVAVSTDTHFTKWAHSSSETAKIKAMIGDPTGALTRNFNDNREDEGLAD 120	QY 1 MSЛNTEIЛSFRATAYKQFVEVSLEAVLKGWAV-FVFPYPADETFVCPTELGDVADHYE 79	
Db 60 VFTRLGVIEVYAVSTDTHFTKWAHSSSETAKIKAMIGDPTGALTRNFNDNREDEGLAD 119	QY 61 ELOKLGVDVAVSTDTHFTKWAHSSSETAKIKAMIGDPTGALTRNFNDNREDEGLAD 120	
QY 121 RATEFWDPOGIIQATEAEGGRASDLRKIAQAYVASHPGEVCPAKKREGEATLAP 180	QY 61 ELOKLGVDVAVSTDTHFTKWAHSSSETAKIKAMIGDPTGALTRNFNDNREDEGLAD 120	
Db 120 RGTFLVDPQGVIQFMEVTAEGIGRNIAELRKIKAAQYVAAPGEVCPAKNEEGKTLAP 179	QY 80 EFQKYGVIEVYAVSTDTHFTKWAHSDSLRKIAQYVASHPGEVCPAKNEEGKTLAP 138	
Qy 181 SLDLVGKI 188	QY 121 RATEFWDPOGIIQATEAEGGRASDLRKIAQAYVASHPGEVCPAKNEEGKTLAP 180	
Db 180 SLDLVGKI 187	Db 139 RGTFLVDPQGVIQFMEVTAEGIGRNIAELRKIKAAQYVAAPGEVCPAKNEEGKTLAP 198	
RESULT 6	Db 199 SLDLVGKI 206	
RESULT 7	F69583	
Db G82668 subunit C of alkyl hydroperoxide reductase XF1530 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: G82668 C;Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing, Nature 405, 151-157, 2000 Ntitle: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: G82668 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-206 <STM>	al kyl hydroperoxide reductase (EC 1.6.4.-) small chain - <i>Bacillus subtilis</i> N;Alternative names: 54K protein; al kyl hydroperoxide reductase chain C22 homolog; NADH C;Species: <i>Bacillus subtilis</i> C;Accession: F69583; G44519 R;Kunst, F.; Ogasawara, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berger, S.; Bourellet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, N;Nature 390, 249-256, 1997 A;Authors: Fouger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallegos, J.; Harwood, C.R.; Henraut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, M; Koettner, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, Y.; Ogawa, K.; Oginara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadbie, Y.; Satoh, T.; Scanlan, A;Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Setiguchi, J.; Sekizawa, A.; Seakeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsitra, P.; Toonouchi, A.; Tosato, V.; Uchiya, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . A;Reference number: A95980; MUID:98044033 A;Accession: F69583 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-187 <KUN> A;Cross-references: GB:Z99124; GB:AU009126; NID:92636442; PIDN:CAB16046.1; PID:926365 A;Experimental source: strain 168 R;Downs, B.C.A. submitted to Genbank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, J.D.; Junqueira, M.L.; Kempfer, E.L.; Kitajima, J.P.; Krueger, C.E.; Kuramitsu, E.E.; Laird, R.; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abranches, M.R.S.; Bureo, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreiro, H.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; as-Neto, E.; Doena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to Genbank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, J.D.; Junqueira, M.L.; Kempfer, E.L.; Kitajima, J.P.; Krueger, C.E.; Kuramitsu, E.E.; Laird, R.; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abranches, M.R.S.; Bureo, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreiro, H.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Valilada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; Reference number: A59328 A;Contents: annotation A;Genetics:	C;Superfamily: alky l hydroperoxide reductase c22 protein; alky l hydroperoxidase c22 p Query Match 68.6%; Score 677.5; DB 2; Length 187; Best Local Similarity 64.9%; Pred. No. 1.7e-54; Matches 122; Conservative 32; Mismatches 33; Indels 1; Gaps 1; C;Key words: NAD; oxidoreductase F;11-14/Domain: alky l hydroperoxidase c22 protein homology <c22>
QY 1 MSЛИNTKIKРPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	QY 1 MSЛИNTKIKРPKNQAKNGEFEITЕKDTЕRWSVFFFPYPADETFVCPTELGDVADHYE 60	

Db 1 MSLIGKEVLPPFREAKNGERIDVNEDLKQKQWSV-FCFWYPADFSVCPTLEDLQEQYA 59
 C; Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
 F; 1-130/Domain: alkyl hydroperoxidase c22 protein homology (fragment) <C22>
 Qy 61 ELOKIGDVYAVSTDHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGLAD 120
 C; Species: Bacillus sp.
 Db 60 ALKELGVEVYVSVTDPFHVKWGHPSSEKISKITYAMIGDPSQTISRNFDVLDLDEETGLAD 119
 Best Local Similarity 63.3%; Score 624.5; DB 2; Length 168;
 Matches 114; Conservative 25; Mismatches 29; Indels 1; Gaps 1;
 Qy 121 RATFVVDPOGIIQAIEVTAEGIGRDAASDLURKIKAAQYVASHPGEVCPAKWKEGEATLAP 180
 Db 120 RGTFITDPGVYIOTVEINAGGIGRDAASLNVKVKAQYVQRNPGEVCPAKWEEGETLIP 179
 Db 181 SLDLVGKI 188
 Db 180 SLDLVGKI 187
 RESULT 8
 F89804 alkyl hydroperoxide reductase subunit c [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 Accession: F89804
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID: 21311952; PMID: 11418146
 A;Accession: F89804
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-189 <KUR>
 A;Cross-references: GB:BA000018; PID:gi13700295; PIDN:BAB41593.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: ahpC
 C;Superfamily: alkyl hydroperoxide reductase subunit c [imported] - Staphylococcus aureus (strain N315)
 Query Match 65.3%; Score 644.5; DB 2; Length 189;
 Best Local Similarity 64.2%; Pred. No. 1.8e-51;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;
 Qy 1 MSLINRKPKRNQAK--KNGEPIETTEKDEPEGRNSVFFFYPADETFVCPTELDQVADH 58
 Db 1 MSLINKEILPFTAQARDPKKQDFKEVQDLSGSV-VCFYPADSFVCPTLEDLQNO 59
 Qy 59 YEELOKLGVYAVASDTHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGL 118
 Db 60 YEELOKLGVYAVASDTHFTHKAWHSSETAKIKYAMIGPTGALTRNFNDNMREDEGL 119
 Qy 119 ADRTFVVDPOGIIQAIEVTAEGIGRDAASDLURKIKAAQYVASHPGEVCPAKWKEATL 178
 Db 120 AQRGFIIDPQGVQASEINADGIGRDASTLAHKIKAAQYVQRNPGEVCPAKWEEAKTL 179
 Qy 179 APSLDLVGKI 188
 Db 180 QPGLDLVGKI 189
 RESULT 9
 PS0179 hypothetical protein (ndh 5' region) - *Bacillus* sp. (fragment)
 C;Species: *Bacillus* sp.
 C;Accession: PS0179 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
 R;Xu, X.; Koyama, N.; Cui, M.; Yamagishi, A.; Nosoh, Y.; Oshima, T.
 J. Biochem. 109, 678-683, 1991
 A;Title: Nucleotide sequence of the gene encoding NADH dehydrogenase from an alkalophile
 A;Reference number: JX0166; MUID: 92011449
 A;Accession: PS0179
 A;Molecule type: DNA
 A;Residues: 1-168 <KUR>
 A;Experimental source: strain YN-1
 RESULT 10
 A35441 alkyl hydroperoxide reductase (EC 1.6.4.-) C22 protein - *Salmonella typhimurium*
 C;Species: *Salmonella typhimurium*
 C;Date: 07-Sep-1990 #sequence_revision 18-Nov-1994 #text_change 19-Oct-1995
 C;Accession: A35441; S07525
 R;Tartaglia, L.A.; Storz, G.; Brodsky, M.H.; Lai, A.; Ames, B.N.
 J. Biol. Chem. 265, 10535-10540, 1990
 A;Title: Alkyl hydroperoxide reductase from *Salmonella typhimurium*. Sequence and homo
 A;Reference number: A35441; MUID: 90285183
 A;Accession: A35441
 A;Molecule type: DNA
 A;Residues: 1-184 <TAG>
 A;Cross-references: GB:J05478
 A;Note: the nucleotide sequence given is inconsistent with Genbank accession J05478
 R;Tartaglia, L.A.; Storz, G.; Ames, B.N.
 J. Mol. Biol. 210, 709-719, 1990
 A;Title: Identification and molecular analysis of oxyR-regulated promoters important
 A;Reference number: S07525; MUID: 90133925
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-21 <TAZ>
 A;Note: part of this sequence, including the amino end of the mature protein, was con
 C;Genetics:
 A;Gene: ahpC
 A;Map position: 13 min
 C;Function:
 A;Description: noncatalytic component of the active enzyme, which protects the cell a
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
 C;Keywords: oxidoreductase
 F;11-146/Domain: alkyl hydroperoxidase c22 protein homology <C22>
 RESULT 11
 S52934 alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - *Staphylococcus aureus* (fragm
 C;Species: *Staphylococcus aureus*
 C;Date: 06-Jun-1995 #sequence_revision 22-May-1998 #text_change 17-Jul-1998

C;Accession: S52934	Qy 181 SDLVGKI 188
R;Through, J. P.; Armstrong-Buisseret, L.; Cole, M.B.; Stewart, G.S.A.B.	
submitted to the EMBL Data Library, February 1995	Db 180 SDLVGKI 187
A;Description: A homologue of the Escherichia coli hydroperoxide reductase Ahpc is inducible by aromatic compounds.	
A;Reference number: S52934	
A;Molecule type: DNA	
A;Residues: 1-179 <THR>	
A;Cross-references: EMBL:X85029	
A;Experimental source: strain RN4220	
C;Genetics:	
A;Gene: ahpc	
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein	
C;Keywords: oxioreductase	
F;1-138/Domain: alkyl hydroperoxidase c22 protein homology <>22>	
Query Match	Score 62.1%; DB 2; Length 179;
Best Local Similarity	63.9%; Pred. No. 1.4e-48;
Matches	115; Conservative 24; Mismatches 38; Indels 3; Gaps 2;
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11 FKNQAF--KNGEFIETEKDETEGRWSVFFFYPADTFVCPTELGVADHYEQLQKIVD 68	
Db 1 FTQAOTDPKQDFKEVQDGFVCPTELEQDQELQEVELQKIVN 59	
Qy 69 YVAVSTDHTHFKAWHSSETAKIKYAMIDGDTGALTRNFNDMREDEGLADRAFVUDP 128	
Db 60 VFSVSTDHTHFKAWHSSETAKIKYAMIDGDTGALTRNFNDMREDEGLADRAFVUDP 119	
Qy 129 OGIIQIALETVTEEGIRDASDLRKTKIAQYVASHPEFVCPKWKEEATLAPSVDLGVKI 188	
Db 120 DGVVQASEINADGIGRADASTLAHKIKAAQYVKNPGEVCPAKWEEGAKTLQPGDLVGKI 179	
RESULT 12	
C83627 alkyl hydroperoxide reductase subunit C PA0139 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa)	
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000	
C;Accession: C83627	
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Ljungquist, S.; Lory, S.; Olson, M.V.	
Nature 406, 959-964, 2000	
A;Title: Complete genome sequence of <i>Pseudomonas aeruginosa</i> PA01, an opportunistic pathogen	
A;Reference number: A82950; MUID:20437337	
A;Accession: C83627	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-187 <STO>	
A;Cross-references: GB:AE004452; GB:AE004091; NID:99945968; PIDN:AAG03529.1; GSPDB:GN001	
A;Experimental source: strain PA01	
C;Genetics:	
A;Gene: ahpc; PA0139	
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein	
RESULT 14	
D71314 residues: 1-187 <STO>	
C;Species: <i>Treponema pallidum</i> subsp. <i>pallidum</i> (<i>syphilis spirochete</i>)	
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 11-Jun-1999	
C;Accession: D71314	
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gorson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Gill, S.; Weidman, J.; Smith, H.O.; Venter, J.C.	
A;Title: Complete genome sequence of <i>Treponema pallidum</i> , the syphilis spirochete.	
A;Reference number: A71250; MUID:98332770	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA	
A;Residues: 1-188 <COL>	
A;Cross-references: GB:AE001227; GB:AE000520; NID:93322797; PIDN:AAC65497.1; PID:9332	
A;Experimental source: strain Nichols	
C;Genetics:	
A;Gene: TP0509	
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein	
Query Match	Score 49.5%; DB 2; Length 188;
Best Local Similarity	49.7%; Pred. No. 3e-37;

QY 2 SLINTRKPKFKNQAFRNGEFTETEKDEGKWSVFFFYPADEFVCPTELGDDADHYEE 61
 ||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 3 SLIGRKVIDFKLPATVGGKFTEVNASIKGSWA-FMFYPADEFVCPTELADLRVPS 61

QY 62 LQKLGDVWAVSTDPFHFTHAWHSSETIARIKIKYAMIGDDTGALTRNFEDNMREDEGLADR 121
 ||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 62 FVEIGCKVSYSTDSKVHKAWADADTNIKLPYEMISDKRAGKLAGFFGVILLPDWHALR 121

QY 122 ATFWVDPGIQIAQIETAEIGGRDASDLRKIKAOYVASHPGEVCPAKWKEGEATLAPS 181
 ||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 122 GTFWVDPEGLVKAFEVHDMSGIGRADELLRKVQSOFVAKIGDQCPARURPKAKTLKPG 181

QY 182 LDLVGKI 188
 ;||:|||
 Db 182 IDLGKTI 188

RESULT 15

70343 alkyl hydroperoxide reductase - Aquifex aeolicus

C;Species: Aquifex aeolicus
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 11-Jun-1999
 C;Accession: G70343
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
 V;Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A;Reference number: A70300; MUID:9819666
 A;Accession: G70343
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-211 <AOF>
 A;Cross-references: GB:AE000692; NID:g2983130; PID:AC06735.1; PID:g2983132; GB:AE00065
 A;Experimental source: strain VF5
 C;Genetics:
 A;Gene: ahcC1
 C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 prot

Query Match 46.1%; Score 455.5; DB 2; Length 211;
 Best Local Similarity 45.0%; Pred. No. 3.6e-34;
 Matches 85; Conservative 41; Mismatches 58; Indels 5; Gaps 3;

QY 4 INTKIKPKFKNQAF- KNGEFIEITEKD- -TEGRWSVFFFYPADEFVCPTELGDDADHY 59
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 Db 18 VGQKVNPNEMETYDPSKGKGVYLEDLKERKW-VILFFYPADYFVCPTELADLAEKY 76

QY 60 EBLQKLGDVWAVSTDPFHFTHAWHSSETIARIKIKYAMIGDDTGALTRNFEDNMREDEGLA 119
 ;||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 77 DELKEMCEVIVSSTDKFVHLWRDPEPLKVNKPMDGPTGQVSRLFVYDENTGLA 136

QY 120 DRATFWVDPGIQIAQIETAEIGGRDASDLRKIKAOYVASHPGEVCPAKWKEGEATLAPS 179
 ;||| :|| | :|| | :|| | :|| | :|| | :|| | :|| |
 Db 137 LRGTFLINPSEGVLVGSEVNFYINVGRNADELVRMKANVYLMSPHEACPAKWPFGKTLK 196

QY 180 PSLDLVGKI 188
 ;||| :|||:
 Db 197 PSEELVGRV 205

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5	
OM protein - protein search, using sw model		
Run on:	May 19, 2002, 00:31:21 ; Search time 40.11 Seconds	(without alignments)
	181.483 Million cell updates/sec	
Title:	US-09-679-705-24	
Perfect score:	987	
Sequence:	MSLINTRKPKFKNQAFKNGE.....AKWKBGEATLAPSILDVKGII 188	
Scoring table:	BLOSUM62	
	Gapop 10.0 , Gapext 0.5	
Database :	SwissProt_40:*	
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
Searched:	105224 seqs, 38719550 residues	
Total number of hits satisfying chosen parameters:	105224	
Minimum DB seq length:	0	
Maximum DB seq length:	200000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing first 45 summaries	
SUMMARIES		
Result No.	Score	Query Match Length DB ID Description
1	965.5	97.8 186 1 AHPC_ECOLI P26427 escherichia
2	958.5	97.1 186 1 AHPC_SALTY P19479 salmonella
3	677.5	68.6 187 1 AHPC_BACSU P80239 bacillus su
4	624.5	63.3 168 1 VNDH_BACSP P26830 bacillus sp
5	366.5	37.1 266 1 BASI_ARATH P06291 arabidopsis
6	362	36.7 210 1 BASI_WHEAT P80202 triticum ae
7	361	36.6 198 1 PDX1_RAT P35704 rattus norv
8	361	36.6 210 1 BASI_HORV P06468 hordeum vul
9	358.5	36.3 198 1 PDX2_MOUSE P06171 mus musculu
10	354	35.9 265 1 PDX1_SP10L P02436 spinacia ol
11	346.5	35.1 256 1 PDX3_HUMAN P30048 homo sapien
12	343.5	34.8 198 1 PDX2_HUMAN P32119 homo sapien
13	338	34.2 199 1 PDX1_RAT P063716 rattus norv
14	337.5	34.2 257 1 PDX3_MOUSE P20108 mus musculu
15	335.5	34.0 257 1 PDX3_BOVIN P35705 bos taurus
16	334	33.8 199 1 PDX1_HUMAN Q06830 homo sapien
17	330.5	33.5 199 1 TDX2_BRUMA Q17172 brugia malai
18	329.5	33.4 200 1 TDX_CNPY Q09384 cynops pyrr
19	329	33.3 199 1 PDX1_MOUSE P35700 mus musculu
20	322.5	32.7 271 1 PDX4_HUMAN Q13162 homo sapien
21	322	32.6 229 1 TDX1_BRUMA P48822 brugia malai
22	32.6	274 1 PDX4_MOUSE Q08807 mus musculu
23	31.6	199 1 YC42_PORPU P51272 porphyra pu
24	31.6	226 1 TDX1_GAEL P021824 caenorhabdi
25	31.1	200 1 Y755_SYN3 Q55674 syncochyst
26	305.5	31.0 199 1 TDX1_TRIBR Q26695 tripanocoma
27	29.5	194 1 TDX_FASHE Q91191 fasciola he
28	29.5	200 1 TDX_ONMY Q9Y7f0 neorhynchus
29	28.9	196 1 TSAL_CANAL P19476 entamoeba h
30	27.0	233 1 CR29_ENTH1 P23161 clostidium
31	26.9	178 1 R20K_CLOPA P49537 odontella s
32	26.5	204 1 YC42_OP0SI Q04120 saccharomyce
33	26.2	
34	250.5	25.4 195 1 TSAL_YEAST
35	249.5	25.3 1 TAA_BUCAI
36	243.5	24.7 1 PDX2_PIG
37	241	24.4 1 TAA_HELPJ
38	241	24.4 198 1 TAA_HELPLY
39	226.5	22.9 215 1 TDXH_SULSO
40	226.5	22.9 216 1 TDXH_PVRHO
41	223	22.4 216 1 TDXH_PVRAB
42	221	22.3 215 1 TDX1_SULME
43	220.5	21.9 215 1 TDXH_ARCFU
44	216.5	21.9 217 1 TDXH_MEJIA
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ALIGNMENTS		
RESULT	ID	1
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ID	AHPC_ECOLI	STANDARD; PRT; 186 AA.
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DT	01-AUG-1992 (Rel. 23, Created)	
DT	01-JUN-1994 (Rel. 29, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (SCRP-23)	
DE	(Sulfate starvation-induced protein 8) (SSB8).	
GN	AHPC OR B0605 OR Z0749 OR ECS0644	
OS	Escherichia coli, and	
OS	Escherichia coli col1 0187:H7.	
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC	Escherichia.	
OX	NCBITaxID=562, 83334;	
RP	[1] RN	SEQUENCE FROM N.A.
RC	STRAIN=K12;	
RX	MEDLINE=92276370; PubMed=1592833;	
RA	Smillie D. A., Hayward R.S., Suzuki T., Fujita N., Ishihama A.; "Locations of genes encoding alkyl hydroperoxide reductase on the physical map of the Escherichia coli K-12 genome.";	
RT	J.Bacteriol. 174:3826-3827(1992).	
RL		
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RP	SEQUENCE FROM N.A.	
RC	STRAIN=K12 / MG1655;	
RX	MEDLINE=97426617; PubMed=9278503;	
RA	Blattner F. R., Plunkett G. III, Bloch C. A., Perna N. T., Burland V., Riley M., Collado-Vides J., Glasner J. D., Rode C. K., Mayhew G. F., Gregor J., Davis N. W., Kirkpatrick H. A., Goeden M. A., Rose D. J., Maurer B., Shao Y.; "The complete genome sequence of Escherichia coli K-12.";	
RT	Science 277:1453-1474(1997).	
RL		
RN	[3]	
RP	SEQUENCE FROM N.A.	
RA	Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Lin D., Fedderspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Roberts D., Schramm S., Davis R. W., Namath A., Oefner P., Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.	
RA	[4]	
RP	SEQUENCE FROM N.A.	
RA	Strain=K12;	
RX	MEDLINE=97061202; PubMed=890532;	
RA	Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Sekii Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horikoshi T.;	
RT	"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";	
RT	DNA Res. 3:137-155(1996).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RC	Strain=O157:H7 / EDL933 / ATCC 700927;	
RX	MEDLINE=21074935; PubMed=11206551;	

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotnick E.J., Davis N.W., Lim A., Dimaranta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J.J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.";
 RL *Nature* 409:529-533 (2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 059952;
 RX MEDLINE=21156231; PubMed=11258796;
 DR EMBL; AE000166; AAC7706.1; -.
 DR EMBL; U82538; AAB4806.1; -.
 DR EMBL; D90702; BAA35244.1; -.
 DR EMBL; D90701; BAA35235.1; -.
 DR EMBL; AE005240; AAG54940.1; -.
 DR EMBL; AP002552; BAB34067.1; -.
 DR PIR; JN0289; JN0289.
 DR HSSP; P30041; 1PRX.
 DR SWISS-2DPAGE; P26427; COLI.
 DR ECO2DBASE; B020_9; 6TH EDITION.
 DR Ecogene; EG11384; ahpc.
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW oxidoreductase; Complete proteome.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 165 165 BY SIMILARITY.
 SQ SEQUENCE 186 AA; 20630 MW; 40CDR2D344CA196B CRC64;

RT antibodies against region 2.2 peptide of RNA polymerase sigma
 RT subunit;"
 RL Biochem. Biophys. Res. Commun. 184:634-639(1992).
 RN [8]
 RP SEQUENCE OF 1-13.

RC STRAIN=K12 / W3110;
 RA Pasquali C., Sanchez J.-C., Ravlier F., Golaz O., Hughes G.J.,
 RA Frutiger S., Pequet N., Wilkins M., Apel R.D., Bairoch A.,
 RA Hochstrasser D.F.;
 RL Submitted (SEP-1994) to the SWISS-PROT data bank.
 RN [9]
 SEQUENCE OF 1-27 AND 69-80.

RC STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298466;
 RA Link A.J., Robison K., Church G.M.;
 RA "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of *Escherichia coli* K-12.";
 RL Electrophoresis 18:1259-1313(1997).
 RN [10]
 RP SEQUENCE OF 1-20.
 RC STRAIN=K12;
 RX MEDLINE=96081923; PubMed=7499381;
 RA Cha M.-K., Kim H.-K., Kim I.-H.;
 RT "Thioredoxin-linked 'thiol peroxidase' from periplasmic space of
 Escherichia coli.";
 J. Biol. Chem. 270:28635-28641(1995).
 RN [11]
 RP SEQUENCE OF 1-10.

RC STRAIN=K12 / MG4100;
 RX MEDLINE=96370830; PubMed=8774726;
 RA Quadroni M., Staudermann W., Kertesz M., James P.;
 RT "Analysis of global responses by protein and peptide fingerprinting
 of proteins isolated by two-dimensional gel electrophoresis's
 Application to the sulfate-starvation response of *Escherichia coli*.";
 RL Eur. J. Biochem. 233:773-781(1996).
 CC -1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
 CC DITHIOL FORM.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- PTM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 H(2)O(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-S-OH) RAPIDLY
 REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
 INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN.
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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 DR EMBL; D13187; BAA02485.1; -.
 DR EMBL; U82538; AAB4806.1; -.
 DR EMBL; D90702; BAA35244.1; -.
 DR EMBL; D90701; BAA35235.1; -.
 DR EMBL; AE005240; AAG54940.1; -.
 DR EMBL; AP002552; BAB34067.1; -.
 DR PIR; JN0289; JN0289.
 DR HSSP; P30041; 1PRX.
 DR SWISS-2DPAGE; P26427; COLI.
 DR ECO2DBASE; B020_9; 6TH EDITION.
 DR Ecogene; EG11384; ahpc.
 DR InterPro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW oxidoreductase; Complete proteome.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT ACT_SITE 165 165 BY SIMILARITY.
 SQ SEQUENCE 186 AA; 20630 MW; 40CDR2D344CA196B CRC64;

Query Match 97.8%; Score 965.5; DB 1; Length 186;
 Best Local Similarity 99.5%; Pred. No. 7. 9e-80; 0; Mismatches 1; Gaps 1;
 Matches 186; Conservative 0; Indels 1; Gaps 1;
 QY 2 SLINTKIKPPKKQAFKNGEFEITEKDEGKGRWSVFFFYPAADFTFCPTSLGDVADHYEE 61
 Db 1 SLINTKIKPKRNQAFKNGEFEITEKDEGKGRWSVFFFYPAADFTFCPTSLGDVADHYEE 59
 QY 62 LQKLGYDVAYSTDTHTHKWHSSETAKIYAMGDPGALTRNFNDNREDEGLADR 121
 Db 60 LQKLGYDVAYSTDTHTHKWHSSETAKIYAMGDPGALTRNFNDNREDEGLADR 119
 QY 122 ATFWVPQGQIAEVTAEGIGRDASSLRKIKAQYVASHPGEVCPAKNKEGEATLAPS 181
 Db 120 ATFWVPQGQIAEVTAEGIGRDASSLRKIKAQYVASHPGEVCPAKNKEGEATLAPS 179
 QY 182 LDLVGKI 188
 Db 180 LDLVGKI 186

RESULT 2
 AHPC-SALTY
 ID AHPC-SALTY STANDARD; PRT; 186 AA.
 AC P19479;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-).
 GN AHPC OR STM0608 OR Smy0633;
 OS *Salmonella typhimurium*, and
 OC *Salmonella typhi*.
 OC *Bacteriia*; *Proteobacteria*; *gamma subdivision*; *Enterobacteriaceae*;
 OC *Salmonella*.
 OX NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=*typhimurium*; STRAIN=TN1379;
 RX MEDLINE=90285183; PubMed=219151;
 RA Tartaglia L.A., Storz G., Brodsky M.H., Lai A., Ames B.N.;
 RT "Alkyl hydroperoxide reductase from *Salmonella typhimurium*. Sequence
 and homology to thioredoxin reductase and other flavoprotein
 disulfide oxidoreductases";
 RL J. Biol. Chem. 265:10535-10540(1990).
 RN [2]
 RP REVISTONS TO C-TERMINUS.
 RC SPECIES=*S. typhimurium*;
 MEDLINE=94316629; PubMed=8041738;

RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RA "Cloning and sequencing of thiol-specific antioxidant from mammalian
 RT brain; alkyl hydroperoxide reductase and thiol-specific antioxidant
 RT define a large family of antioxidant enzymes";
 RT proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=LTA / SGSC1412 / ATCC 700720;
 RC SPECIES=S typhimurium; STRAIN=LTA / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=117609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrelle P.,
 Courtney L., Porwollik S., Ali J.J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LN2";
 RL Nature 413:852-856(2001).
 RN [4]
 RP SEQUENCE OF 1-20 FROM N.A.
 RC SPECIES=S typhimurium;
 RX MEDLINE=90133925; PubMed=2693740;
 RA Tartaglia L.A., Storz G., Ames B.N.;
 RT "Identification and molecular analysis of oxyR-regulated promoters
 RL J. Mol. Biol. 210:709-719(1989).
 RN [5]
 RP SEQUENCE OF 1-24.
 RC SPECIES=S typhimurium; STRAIN=OXYR1;
 RX MEDLINE=89109157; PubMed=2643600;
 RA Jacobson S., Morgan R.W., Christian M.F., Ames B.N.;
 RT "An alkyl hydroperoxide reductase from *Salmonella typhimurium*
 RT involved in the defense of DNA against oxidative damage. Purification
 RT and properties";
 RL J. Biol. Chem. 264:1488-1496(1989).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S typhi; STRAIN=CPIB;
 RX MEDLINE=21534947; PubMed=1167608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks D., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jaelens K.,
 RA Krogh A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar Typhi CPIB.";
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: DIRECTLY REDUCES ALKYL HYDROPEROXIDES WITH THE USE OF
 CC ELECTRONS DONATED BY THE 57 KDA FLAVOPROTEIN ALKYL HYDROPEROXIDE
 CC REDUCTASE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- PTM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN.
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC
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 CC
 DR HSSP; P30041; IPRX.
 DR StyGene; SG10004; apcC.
 DR Interpro; IPR00866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 KW Oxidoreductase; Complete proteome.
 RN INIT_MET 0
 FT ACT_SITE 0
 FT ACT_SITE 46 46 BY SIMILARITY.
 FT ACT_SITE 165 165 BY SIMILARITY.
 FT CONFLICT 1 1 S -> G (IN REF. 5).
 FT CONFLICT 4 4 N -> D (IN REF. 5).
 FT CONFLICT 13 13 O -> N (IN REF. 5).
 FT CONFLICT 16 16 K -> H (IN REF. 5).
 FT CONFLICT 19 19 E -> H (IN REF. 5).
 FT CONFLICT 22 22 E -> S (IN REF. 5).
 SQ 186 AA; 20616 MW; 83d48A7a667FF5DB0 CRC64;

Query	Match	Score	DB	Length
Best Local Matches	Similarity	97.1%	DB 1;	186;
183;	Conservative	97.9%	Pred. No.	3.4e-79;
			Indels	0;
			Gaps	1;
QY	2 SLINTKKPKRNQAFNGEFEITEKDTGEGRNSVFFFYPADFTFCPTELGDVADHEE	61	Db	1 SLINTKKPKRNQAFNGEFEITEKDTGEGRNSVFFFYPADFTFCPTELGDVADHEE 59
OY	62 LQKLGVDVYAVSTDHPTHKAWHSSETITAKIYAMIGDPGALTNRNFNNREDEGLADR	121	Db	60 LQKLGVDVYAVSTDHPTHKAWHSSETITAKIYAMIGDPGALTNRNFNNREDEGLADR 119
OY	122 ATFVVPPQGIIQIAETTAEGGRDASDLRLTIKAQAYVASHPGEVCPAKNKEGEATLAPS	181	Db	120 ATFVVPPQGIIQIAETTAEGGRDASDLRLTIKAQAYVASHPGEVCPAKNKEGEATLAPS 179
OY	182 LDLVGKI 188	Db	180 LDLVGKI 186	
Db	LDLVGKI 186			
RESULT 3	AHPC_BACSU			
ID AHPC_BACSU	STANDARD;			
ID AHPC_BACSU	PRT;	187 AA.		
ID P80239; P53562;				
DT 01-FEB-1995 (Rel. 31. Created)				
DT 01-OCT-1996 (Rel. 34. Last sequence update)				
DT 16-OCT-2001 (Rel. 40. Last annotation update)				
DE Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (General stress DE protein 22).				
GN AHPC.				
OS <i>Bacillus subtilis</i> .				
OC Bacteria; Firmicutes; <i>Bacillus/Clostridium</i> group;				
OC <i>Bacillus/Staphylococcus</i> group; <i>Bacillus</i> .				
OX NCBI_TaxID=1423;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=168;				
RA Kasahara Y., Nakai S., Yoshioka H., Ogasawara N.;				
RA Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.				
RN [2]				
RP SEQUENCE OF 1-41.				
RC STRAIN=168 / YB86;				
RX MEDLINE=94236234; PubMed=8180695;				
RA Hartford O.M., Dowd B.C.A.;				
RT "Isolation and characterization of a hydrogen peroxide resistant RT mutant of <i>Bacillus subtilis</i> ";				
RL Microbiology 140:297-304(1994).				
RN [3]				
RP SEQUENCE OF 1-14.				
RC STRAIN=ISB.				
RC STRAIN=ISB.				
RC MEDLINE=94262319; PubMed=8012595;				
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,				
RA Schmid R., Mach H., Hecker M.;				
RT "Analysis of the induction of general stress proteins of <i>Bacillus</i> RT subtilis";				
DR S07525; S07525.				

RL Microbiology 140:741-752(1994).
 CC -!- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
 CC DITHIOL FORM.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS AND
 CC GLUCOSE LIMITATION.
 CC -!- PTM: THE CYS-47-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H₂O₂(2), AND THE OXIDIZED CYS-47 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-166-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE AhPC/TSA FAMILY.
 CC
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 CC
 DR InterPro; IPR000866; Ahpc-TSA.
 DR EMBL; D78193; BAA1168.1; -.
 DR EMBL; Z99124; CAB16046.1; -.
 DR Sublist; BG11385; ahpc.
 DR DR InterPro; IPR000866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 DR Kw Hypothetical protein; Antioxidant.
 DR EMBL; D10701; BAA0154.1; -.
 DR DR PIR; PS0179; PS0179.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 FT NON_TER 1
 FT ACT_SITE 28 28 BY SIMILARITY.
 FT CONFLICT 8 8 V->WV (IN REF. 3); CRC64;
 SQ SEQUENCE 187 AA; 20627 MW; 10D6643BC90F54E CRC64;

Query Match 68 %; Score 677.5; DB 1; Length 187;
 Best Local Similarity 64.9%; Pred. No. 5.9e-54;
 Matches 122; Conservative 32; Mismatches 33; Indels 1; Gaps 1;

QY 1 MSLINTKIKPKNQARKNGERIEITEKDFTGCRWSVFFFFYPADFTFVCPTELELGVDADHYE 60
 Db 1 MSLIKEKVLPFEAKAFKGNGERIDTVNEDLGQWSV-FCFVPADDSFVCPTELEDLQEQYA 59

QY 61 ELQKLGUDVAVSTDFTHKAWNSSETAKYAMGPTGALTTRNFDRMRDEGLAD 120
 Db 60 ALKELGVEVYVSYSTDTHFKHGWDHSSEKISKITVAMGDPSQTSRNFVLDLDEETGLAD 119

QY 121 RATEVYDVPQSIQTQATEVTAGIGRASDILRKIRKAQYVASHPGVCPAKWKESEATLAPSUDLVKI 180
 b 120 RGTFLIDPDGVQIVTEINAGGIGRDASNLVNVKRAQYVQRNPGEVCPAKWQEGDETLPKPSLDLVKI 179

QY 181 SLDLVGKI 188
 Db 180 SLDLVGKI 187

RESULT 4

YNDB_BACSP STANDARD; PRT; 168 AA.

ID YNDA_BACSP STANDARD; PRT; 168 AA.

AC P26830; DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in NDH 5 region (Fragment).
 OS Bacillus sp. (strain IN-1).
 OC Bacterium; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; Bacillus.

NCBI_TaxId=1409; RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV; COLUMBIA;
 RX MEDLINE=9201149; PubMed=1917890;
 RA Xu X., Koyama N., Cui M., Yamagishi A., Nosoh Y., Oshima T.;
 RT "Nucleotide sequence of the gene encoding NADH dehydrogenase from an alkaliophile, *Bacillus* sp. strain IN-1.";

RL J. Biochem. 109:678-683(1991).
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- PTM: THE CYS-28-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H₂O₂(2), AND THE OXIDIZED CYS-28 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-147-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE AhPC/TSA FAMILY.
 CC
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 CC
 DR EMBL; D10701; BAA0154.1; -.
 DR DR PIR; PS0179; PS0179.
 DR InterPro; IPR000866; Ahpc-TSA.
 DR Pfam; PF00578; Ahpc-TSA; 1.
 FT NON_TER 1
 FT ACT_SITE 147 147 BY SIMILARITY.
 FT SEQUENCE 168 AA; 18479 MW; 2D58C57BB7726DE CRC64;

Query Match 63.3%; Score 624.5; DB 1; Length 168;
 Best Local Similarity 67.5%; Pred. No. 3e-49;
 Matches 114; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 20 EFILETEKDFTGRWSVFFFFYPADFTFVCPTELELGVDADHYEELOKLGVDYAVSTDTHET 79
 Db 1 EFILESEESFKQWSV-LCKYPADFTFVCPTELEDLQENAYAALKELGVEVFSASTDHT 59

QY 80 HKAWNSSETAKYAMGPTGALTTRNFDRMRDEGLADRATEWPDGFIQAEWVA 139
 Db 60 HKGWHDSETITGKTYAMICDQSOTLSRNFDVLNEVGSVGLADRGTFIDPGVWQAENA 119

QY 140 EGIGRADSLILRKIRKAQYVASHPGVCPAKWKESEATLAPSUDLVKI 188
 Db 120 EGIGRDASTLVNKIRKAQYVVRNNPGEVCPAKWQEGDETLPKPSLDLVKI 168

RESULT 5

BASL_ARATH STANDARD; PRT; 266 AA.

ID BASL_ARATH STANDARD; PRT; 266 AA.

AC 096291; P22938; Q9SYV0; DT 01-Nov-1997 (Rel. 35, Created)
 DT 16-Oct-2001 (Rel. 40, Last sequence update)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)

DE 2-CYS peroxiredoxin BASL; chloroplast precursor.
 GN BASL OR AN3G1630 OR T19911.3 OR F24K9.28.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV; COLUMBIA;
 RA Baier M., Dietz K.-J.;
 RT "2-Cys peroxiredoxin basl from *Arabidopsis thaliana*."
 RT (In) Plant Gene Register PGR96-031.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV; COLUMBIA;
 RX MEDLINE=9740890; PubMed=9263459;
 RA Baier M., Dietz K.-J.;
 RT "The Plant 2-Cys peroxiredoxin BASL is a nuclear-encoded chloroplast protein: its expressional regulation, phylogenetic origin, and implications for its specific physiological function in plants.";

RP	REVISIONS.	[3]
RA	Baier M.;	
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	
RP	SEQUENCE FROM N.A.	[4]
RC	STRAIN=CV; COLUMBIA;	
RX	MEDLINE=21016720; PubMed=11130713;	
RA	Salancibut M., Lemcke K., Rieger M., Ansorge W., Unseld M.,	
RA	Fartmann B., Waller G., Bloecker H., Perez-Alonso M., Obermaier B.,	
RA	Deisney M., Boutry M., Grivel L.A., Mache R., Puigdomenech P.,	
RA	De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,	
RA	Winkler P., Cattolico L., Weissbach H., Saarlin W., Quettier F.,	
RA	Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,	
RA	Wurmback E., Drzonek H., Erfle H., Jordan N., Bangert S.,	
RA	Vezzi A., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,	
RA	Conrad A., Hornischer K., Kauer G., Topps S., Simionati B.,	
RA	Pichelt J., Schafre M., Schoen O., Bargues M., Terol J., Nordsiek G.,	
RA	Navarro P., Colliado C., Perez-Perez A., Ottewaelde B., Duchemin D.,	
RA	Cooke R., Laude M., Berger-Llauro C., Purnelle B., Masuy D.,	
RA	de Haan M., Marise A.C., Alcaraz J.-P., Coette A., Casacuberta E.,	
RA	Monfort A., Argiroli A., Flores M., Iuguori R., Vitale D.,	
RA	Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,	
RA	Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Fallon L.J., Jenkins J.,	
RA	Rooney T., Rizzo M., Waltz A., Utterback T., Fujii C.Y., Shear T.P.,	
RA	Creasy T.H., Haas B., Maihi R., Wu D., Peterson J., van Aken S.,	
RA	Pai G., Millscher J., Sellers P., Gill J.E., Heldbyum T.V.,	
RA	Preuss D., Lin X., Niemann W.C., Salberg S.L., White O., Venter J.C.,	
RA	Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,	
RA	Sasamoto S., Kimura T., Idosawa K., Kawashima K., Kishida Y.,	
RA	Kiyokawa C., Kohara M., Matsuno A., Muraki A.,	
RA	Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,	
RA	Watanahe A., Yamada M., Yasuda M., Tabata S.;	
RT	"Sequence and analysis of chromosome 3 of the plant <i>Arabidopsis thaliana</i> ."	
RL	Nature 408:820-822(2000).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RA	Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,	
RA	Ecker J.;	
RT	"Full length cDNA sequence of <i>Arabidopsis thaliana</i> ."	
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.	
CC	-i- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF. INVOLVED IN THE DETOXIFICATION OF ALKYL HYDROPEROXIDES. EXPRESSION IS REPRESSION IN INDUCED BY OXIDATIVE STRESS.	
CC	-i- SUBUNIT: HOMODIMER (BY SIMILARITY).	
CC	-i- SUBCELLULAR LOCATION: CHLOROPLAST.	
CC	-i- PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY H ₂ O ₂ , AND THE OXIDIZED CYS-119 (PROBABLY CYS-SOH) RAPIDLY REACTS WITH CYS-241-SH OF THE OTHER SUBUNIT TO FORM AN INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE REDUCED BY THIOREDOXIN (BY SIMILARITY).	
CC	-i- SIMILARITY: BELONGS TO THE AHP/C/TSA FAMILY.	
CC		
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CC		
DR	ENBL: X94218; CA63909.1; -	
DR	EMBL: Y1078; CAAT1503.1; -	
DR	EMBL: X97910; CAN66484.2; -	
DR	AC005918; AAC02131.1; -	
DR	AC008153; AAG51430.1; -	
DR	AFA324996; AAG40348.1; -	
DR	HSSP: P30041; 1PRX.	
DR		
DR	Interpro, IPR000866, AHP/C-TSA.	
DR	PFam: PF00578; AHP-C-TSA; 1.	
DR	Antioksidant; Chloroplast; Transit peptide.	
FT	TRANSIT 1	65
FT	CHAIN 66	266
FT	ACT_SITE 119	119
FT	ACT_SITE 241	241
FT	CONFICT 83	83
FT	E -> K (IN REF. 1).	
FT	I -> N (IN REF. 1 AND 2).	
FT	CONFICT 122	122
FT	MISSING (IN REF. 1).	
FT	CONFICT 192	192
FT	I -> IGI (IN REF. 2).	
FT	CONFICT 233	235
FT	IOE -> TG (IN REF. 1).	
FT	CONFICT 247	247
FT	P -> S (IN REF. 1).	
SQ	SEQUENCE 266 AA; 29092 MW; 2ZCEB476A1A8694AD CRC64;	
RESULT	6	
ID	BASL_WHEAT	
ID	BASL_WHEAT	
STANDARD:		
PRT:	210 AA.	
DT	P80602;	
DT	01-OCT-1995 (Rel. 34, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	2-CYS peroxiredoxin BASL, chloroplast precursor (thiol-specific antioxidant protein) (Fragment).	
DE	TSA.	
GN		
OS	Triticum aestivum (wheat).	
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
OC	Triticeae; Triticum.	
NCBI_TaxId=4565;		
RN	[1]	
SEQUENCE FROM N.A.		
RA	TSunoyama Y., Toyoshima Y.;	
RA	Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.	
RN	[2]	
SEQUENCE OF 11-35.		
RC	STRAIN=CV; NOURIN 61; TISSUE=leaf;	
RA	TSunoyama Y., Takashi S.; Toyoshima Y.;	
RA	Submitted (MAY-1996) to the SWISS-PROT data bank.	
CC	-i- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF.	
CC	-i- SUBUNIT: HOMODIMER (BY SIMILARITY).	
CC	-i- SUBCELLULAR LOCATION: Chloroplast.	
CC	-i- PTM: The CYS-64-SH group is the primary site of oxidation by H ₂ O ₂ , and the oxidized CYS-64 (probable CYS-SOH) rapidly reacts with CYS-185-SH of the other subunit to form an intermolecular disulfide. This disulfide might subsequently be reduced by thioredoxin (by similarity).	
CC	-i- SIMILARITY: BELONGS TO THE AHP/C-TSA FAMILY.	

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CC DR EMBL; AB000405; BAA19099.1; -.

CC DR HSSP; P30041; 1PRX.

CC DR InterPro; IPR00866; Ahpc-TSA.

CC DR Pfam; PF00578; Ahpc-TSA; 1.

CC CC KW antioxidant; Chloroplast; Transit peptide.

CC FT NON_TER 1 1

CC FT TRANSIT <1 10 CHLOROPLAST.

CC FT CHAIN 1 1 210 2-CYS PEROXIREDOXIN BAS1.

CC FT ACT_SITE 6 6 64 BY SIMILARITY.

CC FT ACT_SITE 185 185 BY SIMILARITY.

CC SQ SEQUENCE 210 AA; 23326 MW; E2D48179D6937E6 CRC64;

Query Match 36.7%; Score 362; DB 1; Length 210; Best Local Similarity 38.3%; Pred. No. 1.5e-25; Matches 70; Conservative 37; Mismatches 72; Indels 4; Gaps 2; Qy 1 NSLINTKIKPFNQAFKNGFEITEKDEGRASVFFFYPADFTVCPTELGVDVADHE 60 Db 17 LPLVGNNKAPDFAAEAVDQEFINVNLSDYIGKVKVILFFYPLDFTFVCPTEIAFSDRHE 76 Qy 61 ELQKLGVYVAYSTDHTHAKW--HSSETAKIKAMIGPTGALTNRNFNDNMREDG 117 Db 77 EFEKINTELGVSVDVFSLAWQTERKSGGLDKYPLVSDVTKSISFGVLIPDG 136 Qy 118 LADRATVWDQGIIQAIETVTAECIGIGRDAASDLIRLKKAQYASHPGEVCPAKWKEGET 177 Db 137 IALRGFLIIDIKGVIHQHSTINNLIGRSDVDETLTRALQVY-KKPDEVCPAGWKPGERS 195 Qy 178 LAP 180 Db 196 MRP 198

RESULT 7

ID PDX2_RAT STANDARD; PRT; 198 AA.

ID AC P35704; PRT; 198 AA.

DT 01-JUN-1994 (Rel. 29, Created)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

Peroxiredoxin 2 (thioredoxin peroxidase 1) (thiol-specific antioxidant protein) (TSA).

PRDX2 OR TPX1.

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TAXID=10116; [1]

RN 1

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RC MEDLINE=94316629; Pubmed=8041738;

RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;

RT "Cloning and sequencing of thiol-specific antioxidant from mammalian brain: alkyl hydroperoxide reductase 1".

RT define a large family of antioxidant enzymes.";

RL Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).

CC -!- FUNCTION: Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2).

CC -!- SUBUNIT: Homodimer, disulfide-linked, upon oxidation (by

CC DR EMBL; AB000405; BAA19099.1; -.

CC DR HSSP; P30041; 1PRX.

CC DR InterPro; IPR00866; Ahpc-TSA.

CC DR Pfam; PF00578; Ahpc-TSA; 1.

CC CC KW antioxidant. BY SIMILARITY.

CC FT ACT_SITE 172 172 BY SIMILARITY.

CC FT ACT_SITE 172 172 BY SIMILARITY.

CC SQ SEQUENCE 198 AA; 21784 MW; FC6AD9B0E904447B CRC64;

Query Match 36.6%; Score 361; DB 1; Length 198; Best Local Similarity 40.3%; Pred. No. 1.7e-25; Matches 73; Conservative 35; Mismatches 65; Indels 8; Gaps 4; Qy 9 KP--TRNQAFKNGFEITEKDEGRASVFFFYPADFTVCPTELGVDVADHEEQLK 65 Db 10 KPADPDFGTAVVDGAFREKILSDYRGKV-VVLFYPLDFTFVCPTEIAFSDHAEDFRKL 68 Qy 66 GVDVYAVSTDHTHAKWHSSET--IATIKYAMIGDPGTGALTNRNFNDNMREDGADRA 122 Db 69 GCEVLGVSVDSQFTHLAWINTPRKEGLGPLNTPLADVTKSLSONGYVLRKNDIEGARY 128 Qy 123 TPVVDQGIIQAIETVTAECIGIGRDAASDLIRLKKAQYASHPGEVCPAKWKEGETAPSL 182 Db 129 LFLLIDAKGVLQITVNDLPVGRSEARLYQAFQYDEH-GEVCPAGWKPGESDTIKPNV 187 Qy 183 D 183 Db 188 D 188

RESULT 8

ID BAS1_HORVU STANDARD; PRT; 210 AA.

ID BAS1_HORVU PRT; 210 AA.

AC Q96468; PRT; 210 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

2-cys peroxiredoxin BAS1, chloroplast precursor (thiol-specific antioxidant protein) (Fragment).

DE DE

GN GN

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; OX NCBI_TAXID=4513; RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Cv; GERBER; TISSUE=leaf; PRT; 210 AA.

RC MEDLINE=94316629; Pubmed=8041738;

RA Baier M., Dietz K.-J.;

RT "Primary structure and expression of plant homologues of animal and fungal thioredoxin-dependent peroxide reductases and bacterial alkyl hydroperoxide reductases.";

RT Plant Mol. Biol. 31:553-564(1996).

CC -!- FUNCTION: May be an antioxidant enzyme particularly important in

CC or send an email to license@ib-sib.ch).

RX MDDLINE=93162043; PubMed=1286667;

RA Rasmussen H., van Damme J., Puype M., Geser B., Cellis J.E.,

DR Vandekerckhove J.,

DR EMBL; BC002685; AHH2685;1; -

DR EMBL; T10522; -; NOT_ANNOTATED_CDS.

DR HSSP; P30041; IPRX.

DR SWISS-2DPAGE; P30048; HUMAN.

DR Sienna-2DPAGE; P30048; -.

DR Pfam; PF00578; AhPC-TSA; 1.

DR Antioxidant; Mitochondrion; Transit peptide.

FT TRANSIT 1 62 MITOCHONDRION.

FT CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.

FT ACT_SITE 108 108 BY SIMILARITY.

FT ACT_SITE 229 229 BY SIMILARITY.

SQ SEQUENCE 256 AA; 27692 MW; 8BEB7/F5E55BF9E CRC64;

RC TISSUE=Colon carcinoma;

RX MEDLINE=91295306; PubMed=9150948;

RA JI H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;

RT "A two-dimensional gel database of human colon carcinoma proteins.";

RL Electrophoresis 18:605-613(1997).

CC - FUNCTION: Reduces peroxides with reducing equivalents provided

CC through the thioredoxin system. It is not able to receive

CC electrons from glutaredoxin. May play an important role in

CC eliminating peroxides generated during metabolism. Might

CC participate in the signaling cascades of growth factors and tumor

CC necrosis factor-alpha by regulating the intracellular

CC concentrations of H₂O₂.

CC - FUNCTION: Enhances natural killer (NK) cells activity

CC - SUBUNIT: Homodimer; Disulfide-linked, upon oxidation (by

CC similarity).

CC - SUBCELLULAR LOCATION: Cytoplasmic.

CC - PIM: The Cys-51 SH group is the primary site of oxidation by

CC H₂O₂, and the oxidized Cys-51 (probably Cys-SOH) rapidly

CC reacts with Cys-172-SH of the other subunit to form an

CC intermolecular disulfide. This disulfide might subsequently be

CC reduced by thioredoxin (by similarity).

CC -1- SIMILARITY: BELONGS TO THE AHPC-TSA FAMILY.

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CC

DR EMBL; Z22548; CAA80269;1; -

DR EMBL; L19185; AAC50465;1; -

DR EMBL; X82321; CAA57764;1; -

DR HSSP; P30041; IPRX

DR SWISS-2DPAGE; P32119; HUMAN.

DR Arrhus/Ghent-2DPAGE; 6116; IEF.

DR MM; 600538; -

DR InterPro; IPR008866; AhPC-TSA.

DR Pfam; PF00578; AhPC-TSA; 1.

FT ACT SITE 172 172 BY SIMILARITY.

FT ACT SITE 172 172 BY SIMILARITY.

FT CONFLICT 59 66 SNRAEDER -> TTVKRTSA (IN REF. 1).

FT CONFLICT 82 82 T -> N (IN REF. 2).

FT CONFLICT 105 105 A -> G (IN REF. 2).

FT CONFLICT 120 120 T -> N (IN REF. 1).

FT CONFLICT 175 175 G -> A (IN REF. 1).

FT CONFLICT 180 180 S -> R (IN REF. 1).

SQ SEQUENCE 198 AA; 21892 MW; 1AC781D908B32B46 CRC64;

Query Match 35.1%; Score 346.5; DB 1; Length 256;

Best Local Similarity 40.2%; Pred. No. 4 6e-24;

Matches 70; Conservative 33; Mismatches 66; Indels 5; Gaps 3;

RA Oberbaumer I.;

RA Submitted (Oct-1996) to the EMBL/GenBank/DDJB databases.

[4] SEQUENCE OF 17-25; 140-150 AND 163-185.

RC TISSUE-Keratinocytes;

QY	5	NARIKIKD--FKNQAFKNGEETEKEOTEGRMSVFVFFYPADFTFCPTTELGDVADHYE	34.2%; Score 338; DB 1; Length 199;
Db	5	NARIKIKD--FKNQAFKNGEETEKEOTEGRMSVFVFFYPADFTFCPTTELGDVADHYE	34.2%; Score 338; DB 1; Length 199;
QY	61	ELOKLGVYAVSTDTHFTKAWHSSET--IARIKYAMIGDTGALIRNFNDRMEDRE 63	Query Match 34.2%; Score 338; DB 1; Length 199;
Db	64	DPRKLGSCEVLGVYVSQDFTHLWINTPKEGGLGPLNPLADVTRISDEGYVLUKE 123	Best Local Similarity 36.6%; Pred. No. 2e-23; Matches 70; Conservative 70; Mismatches 10; Indels 10; Gaps 5;
QY	118	IADRATFVVDPGIGIQQIAEVTTAEGIGRDAASDLRKIRKAQYASHPGEVCAPKWKEGAT 177	Query Match 34.2%; Score 338; DB 1; Length 199;
Db	124	IAYRGLFLIDKGVLQRQITVNDLPVGRSVDEALRLVQAFQYDEH-GEVCPAGWPGSDDT 182	Best Local Similarity 36.6%; Pred. No. 2e-23; Matches 70; Conservative 70; Mismatches 10; Indels 10; Gaps 5;
QY	178	LAPSLD 183	Query Match 34.2%; Score 338; DB 1; Length 199;
Db	183	iRPNV 188	Best Local Similarity 36.6%; Pred. No. 2e-23; Matches 70; Conservative 70; Mismatches 10; Indels 10; Gaps 5;
RESULT 13			
PDX1_RAT		STANDARD;	PRT; 199 AA.
PDX1_RAT		STANDARD;	PRT; 199 AA.
063716;			01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Peroxiredoxin 1 (thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Heme-binding 23 kDa protein) (HBP23).		
GN	PRDX1 OR TPPX2.		
OS	Rattus norvegicus (Rat).		
OC	Bukarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI_TAXID=10116;		
RN	[1] SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=liver;		
RX	MEDLINE=96072454; PubMed=577920;		
RA	Iwahara S.-I., Satoh H., Song D.-X., Webb J., Burlingame A.L., Nagae Y., Muller-Eberhard U., Purification, characterization, and cloning of a heme-binding protein (23 kDa) in rat liver cytosol. ";		
RA	Biochemistry 34:13398-13406(1995).		
CC	-1- FUNCTION: Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2).		
CC	-1- SIMILARITY: Homodimer; Disulfide-linked, upon oxidation (by reduction by thioredoxin (by similarity)).		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-1- PTM: The CYS-52-SH group is the primary site of oxidation by H(2)O(2), and the oxidized CYS-52 (probably CYS-SOH) rapidly reacts with CYS-173-SH of the other subunit to form an intermolecular disulfide. This disulfide might subsequently be reduced by thioredoxin (by similarity).		
CC	-1- SIMILARITY: Belongs to the AHPc/TSA family.		
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CC	EMBL; D30035; BAA06275_1.		
CC	DR	InterPro; IPR00866; AhpC-TSA.	
CC	DR	PFam; PF00578; AhpC-TSA.	
CC	DR	Antioxidant.	
CC	ACT_SITE 52 52 BY SIMILARITY.		
CC	FT ACT SITE 173 173 BY SIMILARITY.		
CC	SEQUENCE 199 AA; 22109 MW; BDFFD4ABA8A77FDA CRC64;		
CC	DR	DR	
CC	EMBL; M28723; AA039524_1; -.		
CC	DR	PIR; JQ0064; JQ0064.	
CC	DR	RSP; P30041; IPRX.	
RESULT 14			
PDX3_MOUSE		STANDARD;	PRT; 257 AA.
PDX3_MOUSE		STANDARD;	PRT; 257 AA.
ID	P20108;		
AC	P20108;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	01-MAR-2002 (Rel. 41, Last annotation update)		
DE	Thioredoxin-dependent peroxide reductase, mitochondrial precursor (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER5 protein)		
DE	(PRX III).		
DE	PRDX3 OR AOP1 OR MER5.		
GN			
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TAXID=10090;		
RN	[1] SEQUENCE FROM N.A.		
RP	MEDLINE=90060782; PubMed=2583515;		
RA	Yamamoto T., Matsui Y., Natori S., Obinata M.; preferentially expressed in murine erythroleukemia cells. ";		
RA	RT "Cloning of a housekeeping-type gene (MER5) preferentially expressed in murine erythroleukemia cells. ";		
RL	Gene 80:337-343(1989).		
CC	-1- FUNCTION: Thioredoxin-dependent peroxide reductase. Protects radical-sensitive enzymes from oxidative damage by a radical-generating system (by similarity).		
CC	-1- SUBUNIT: Homodimer; Disulfide-linked, upon oxidation (by similarity).		
CC	-1- SUBCELLULAR LOCATION: Mitochondrial (Potential).		
CC	-1- TISSUE SPECIFICITY: Housekeeping-type gene preferentially expressed in murine erythroleukemia (MEL) cells.		
CC	-1- INDUCTION: Expression is increased after induction of MEL cells to differentiation by DMSO.		
CC	-1- PTM: The CYS-109-SH group is the primary site of oxidation by H(2)O(2), and the oxidized CYS-109 (probably CYS-SOH) rapidly reacts with CYS-230-SH of the other subunit to form an intermolecular disulfide. This disulfide might subsequently be reduced by thioredoxin (by similarity).		
CC	-1- SIMILARITY: Belongs to the AHPc/TSA family.		
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CC	EMBL; M28723; AA039524_1; -.		
CC	DR	DR	
CC	PIR; JQ0064; JQ0064.		
CC	RSP; P30041; IPRX.		

Mon May 20 10:35:10 2002

us-09-679-705-24.rsp

GenCore version 4.5
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On protein - protein search, using sw model

Run on: May 19, 2002, 00:37:01 ; Search time 97.3 Seconds
(without alignments)

334.255 Million cell updates/sec

Title: US-09-679-705-24
Perfect score: 987

Sequence: 1 MSINTKIKPKFKNAQFKNGE.....AKWKEGEATLAPSLLDVGKI 188

Scoring table: BLOSUM62 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_orphanelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp Rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: spUnclassified:*
- 15: sp_virus:*
- 16: sp_bacteriapl:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	RESULT ID	1	PRELIMINARY;	PRT;	187 AA.
1	742.5	75.2	187	16	Q94B8	094B8	Q94B8				
2	719.5	72.9	187	2	082663	094bb caulobacter	Q94B8; DT	01-JUN-2001 (TREMBLrel. 17, Created)			
3	714	72.3	206	16	09pd49	08863 pseudomonas	DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
4	687.5	69.7	187	2	Q9H10	09pd49 xylella fas	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
5	662	67.1	188	2	087200	09H10 thermus aqu	DE	ALKYL HYDROPEROXIDE REDUCTASE, SUBUNIT C.			
6	644.5	65.3	189	16	053647	087200 amphicill	GN	CC2918.			
7	631.5	64.0	188	2	098072	053647 staphylococ	RA	Caulobacter crescentus'.			
8	629	63.7	186	16	Q99XR7	098072 bacteoides	RA	Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;			
9	626	63.4	186	2	06265	099xr7 streptococc	RA	Caulobacter crescentus.			
10	605.5	61.3	187	16	Q91623	06265 streptococc	RA	SEQUENCE FROM N.A.			
11	603.5	61.1	187	16	Q9CIL9	091623 pseudomonas	RA	STRAIN=ATCC 19089 / CB15;			
12	589.5	59.7	187	2	006464	09cili9 lactococcus	RA	MEDLINE=21176998; PubMed=11259647;			
13	563.5	57.1	187	2	030738	06464 xanthomonas	RA	Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., Debay R.T., Dodson R.J., Durkin A.S., Gwynn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J.J., Berry K., Utterback T., Tran K., Wolf A., Yamathavan J., Embley M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus.", DR			
14	488.5	49.5	188	16	093522	09H10 thermus aqu	DR	EMBL: AE005936; AAC24880.1; -			
15	455.5	46.1	186	16	066779	087200 streptococc	DR	TIGR: CC2918; -			
16	385	39.0	174	17	Q97C80	099xr7 streptococc	DR	InterPro: IPR00866; APc-TSA; 1.			
					SQ	097C80 thermoplas	Pfam; PRO0578; ApC-TSA; 1.	Complete proteome.			
					SEQUENCE	097C80 thermoplas	SEQUENCE	187 AA;	2027 MW:	3079FAB56293CD37 CRC64;	

Query Match 75.2%; Score 742.5; DB 16; Length 187;
Best Local Similarity 72.3%; Pred. No. 5.4e-61; Mismatches 27; Indels 1; Gaps 1;
Matches 136; Conservative 27; MisMatches 24; Del 1; Gaps 1;
QY 1 MSINTKIKPKFKNAQFKNGEFILETEKIDEGRSVFFPYADFTFVCPTELGDVADIVE 60

Db	1	MSLINTKPKPKNAQKFEEFETEKEDEGKRSVFFFYPADEPTFCPTEGDVAHYE 60	GN	XE1530.
OY	61	ELQKLGVYVAVSTDTHTHKAWHSSETIATKIKYAMGDPGALTRNFDRNREDEGLAD 120	OS	Xylella fastidiosa.
Db	60	MSLINTKPKPKNAQKFEEFETEKEDEGKRSVFFFYPADEPTFCPTEGDVAHYE 60	OC	Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OY	61	ELQKLGVYVAVSTDTHTHKAWHSSETIATKIKYAMGDPGALTRNFDRNREDEGLAD 120	OC	Xylella.
Db	60	VFTRLGVYEVIAVNSTDHFSRHMADSPAKIKYIWMGDQVNNFEIMRPGGLAD 119	OX	NCBII_TaxID=2371;
OY	121	RATFVVDPGQIQIAEVTAEGGRDASDLRKTKAAQYVASHRGVECPAKWKEGEATLAP 180	RP	SEQUENCE FROM N.A.
Db	120	RGTFLVDPQGVIFMVEVTAEGIGRNAILRKKAQYVAHPGEVCPAKWEGEATLAP 179	RC	STRAIN=9A5C;
OY	181	SLDVVKI 188	RX	MEDLINE-20365717; PubMed=10910347;
Db	180	SLDVVKI 187	RA	Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Accencio M.,
RESULT	2		RA	Barros M.H., Bonacorsi E.D., Bordim S., Bove J.M., Briones M.R.S.,
ID	082863	PRELIMINARY; PRT; 187 AA.	RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
AC	082863;	PRT; 187 AA.	RA	Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
DT	01-NOV-1998 (TREMBlre. 08, Last sequence update)		RA	Contiinho L.L., Cristoffani M., Dias-Neto E., Docena C., El-Dorry H.,
DT	01-JUN-2001 (TREMBlre. 17, Last annotation update)		RA	Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
DE	AHPC.		RA	Fraga J.S., Franca S.C., Franco M.C., Froime M., Furian L.R.,
GN	AHPC.		RA	Garnier M., Goldman S.L., Goldman M.H.S., Gomes S.L., Gruber A.,
OS	Pseudomonas putida.		RA	Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;		RA	Krieger J.E., Kuramae E.E., Laioret F., Lambais M.R., Leite L.C.C.,
OC	Pseudomonas		RA	Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
NCBI_TAXID=303;			RA	Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
[1]			RA	Marques M.V., Martins E.B.A., Martins E.M.F., Matsukuma A.Y.,
RN			RA	Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RP	SEQUENCE FROM N.A.		RA	Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RC	STRAIN=TOL;		RA	Nanni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA	Fukumori F., Horikoshi K.;		RA	de Oliveira M.C., de Oliveira R.C., Palmeiro D.A., Paris A.,
RT	"Toluene Induced Constitutive Overexpression of An Alkyl Hydroperoxide Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of the ahp genes.";		RA	Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RT	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		RA	Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RL	EMBL; AB016689; BAA31468.1; -		RA	de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Savasaki H.E.,
DR	HSSP; P30041; IPRX.		RA	da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
DR	InterPro; IPR000866; Ahpc-TSA.		RA	da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza M.H.,
DR	Pfam; PF00578; Ahpc-TSA; 1		RA	de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchako M.H.,
DR	PRK; PRK00578; Ahpc-TSA; 1		RA	Valida H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
DR	EMBL; AB003983; AFB84339.1; -		RA	Zago M.A., Zattz M., Meléndez J., Setubal J.C.;
DR	HSSP; P30041; IPRX.		RT	"The genome sequence of the plant pathogen Xylella fastidiosa.";
DR	KW		RL	Nature 406:151-155(2000).
SQ	SEQUENCE 187 AA; 20507 MW; CC6351406B9C8168 CRC64;		DR	EMBL; AB003983; AFB84339.1; -
RESULT	3		DR	HSSP; P30041; IPRX.
ID	09PD49	PRELIMINARY; PRT; 206 AA.	DR	Complete proteome.
AC	09PD49;		DR	KW
DT	01-OCT-2000 (TREMBlre. 15, Created)		DR	SEQUENCE 206 AA; 22891 MW; AF703BDE833698D6 CRC64;
DT	01-OCT-2000 (TREMBlre. 15, Last sequence update)		DR	Query Match 72.9%; Score 719.5; DB 2; Length 187; Best Local Similarity 67.6%; Pred. No. 7.3e-59; Matches 127; Conservative 34; Mismatches 26; Indels 1; Gaps 1;
DT	01-DEC-2001 (TREMBlre. 19, Last annotation update)		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DE	SUBUNIT C OF ALKYL HYDROPEROXIDE REDUCTASE.		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
GN			DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
ID	09K110	PRELIMINARY; PRT; 187 AA.	DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
AC	09K110;		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DT	01-OCT-2000 (TREMBlre. 15, Created)		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DT	01-OCT-2000 (TREMBlre. 15, Last sequence update)		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DE	PEROXIREDOXIN.		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
GN			DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
ID	09K110	PRELIMINARY; PRT; 187 AA.	DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
AC	09K110;		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DT	01-OCT-2000 (TREMBlre. 15, Last sequence update)		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DT	01-DEC-2001 (TREMBlre. 19, Last annotation update)		DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
DE			DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;
GN			DR	Query Match 72.3%; Score 714; DB 16; Length 206; Best Local Similarity 69.1%; Pred. No. 2.7e-58; Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;

OS	thermus aquaticus.
OC	Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
OX	NCBI_TaxID=271;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20459059; PubMed=10862622;
RA	Logan C., Mayhew S.G.;
RT	"Cloning, overexpression, and characterization of peroxiredoxin and
RL	NADH peroxiredoxin reductase from <i>Thermus aquaticus</i> .";
DR	J. Biol. Chem. 275:30019-30028(2000).
SQ	SEQUENCE 187 AA; 20982 MW; F4D33C459P104819 CRC64;
RESULT	5
087200	PRELIMINARY; PRT; 187 AA.
ID	087200
AC	087200;
DT	01-NOV-1998 (TREMBlrel. 08, Created)
DT	01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C (EC 1.6.4.-).
GN	AHC OR SA036 OR SAV0381.
OS	Staphylococcus aureus
OS	Staphylococcus aureus (strain N315), and
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Bacillus/Staphylococcus group; Staphylococcus.
OX	NCBI_TaxID=1280, 158879, 158878;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus; STRATN=RNA220;
RX	MEDLINE=96004465; PubMed=1151034;
RA	Armstrong-Buisseret L., Cole M.B., Stewart G.S.;
RT	"A homologue to the <i>Escherichia coli</i> alkyl hydroperoxide reductase AhpC is induced by osmotic upshock in <i>Staphylococcus aureus</i> .";
RL	Microbiology 141:1655-1661(1995).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus; STRAIN=RM4220;
RA	Jones E.C., Francis K.P., Stewart G.S.A.B.;
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX	MEDLINE=21311952; PubMed=11418166;
RA	Kuroda M., Ono T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki T., Nagai Y., Liyan J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani T., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
RA	Sekiimizu K., Hirakawa S., Kubara S., Goto J., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hatajiri M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant <i>Staphylococcus aureus</i> "; Lancet 357:1225-1240(2001).
RL	CC -1- DIITHIOL FORM (BY SIMILARITY).
CC	-1- INDUCTION: BY OSMOTIC UPSHOCK.
CC	-1- SIMILARITY: BELONGS TO THE AHPC-TSA FAMILY.
DR	EMBL; U92441; AAB51151.1; -
DR	EMBL; AB003330; BAB41533.1; -
DR	EMBL; AP003359; BAB56543.1; -
DR	InterPro; IPR000866; AHPC-TSA.
DR	Pfam; PF00578; AHPC-TSA; 1.
SQ	SEQUENCE 188 AA; 20774 MW; E61BA53C0215BAB4 CRC64;
Query Match	67.1%; Score 662; DB 2; Length 188;
Best Local Similarity	63.0%; Pred. No. 1 6e-53;
Matches	119; Conservative 33; Mismatches 35; Indels 2; Gaps 2;
Qy	1 MS LIN KI KPK KQ AF KG NG - ER IE TE K D T G C R W S V F F V P A D F F V C P T E L G D V A D H 59
Db	1 MSL IN KI KPK KQ AF KG NG - KNG E IE TE K D T G C R W S V F F V P A D F F V C P T E L G D V A D H 59
Qy	60 EEL Q K G V D V V A V S T D H F T H K I K A W H S S E T T A K I K A V A M G D P T G A L T R N F D M R E D E G L A 119
DB	60 AE KK LGW EVY S V S T D H F V K A W H S S P A V G S I E V I N M G D S Q T I S Q F D V I N E E G L A 119
Qy	120 D R A T F V W P O G I T O A I E T A G I R D A S D L R I K A Q Y V A S H P G E V C P A K W E G E A T L A 179
Db	120 D R G T F I I D P G V I Q A T E N A D G I G R D A S T L I N K V K A Q V R E N P G E V C P A K W E G E G E T L K 179
Qy	180 P S L D I V G K I 188
Db	180 P S L D I V G K I 188
RESULT	6
053647	PRELIMINARY; PRT; 189 AA.
ID	053647
AC	053647;
DT	01-NOV-1996 (TREMBlrel. 01, Created)
DT	01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C (EC 1.6.4.-).
GN	AHC OR SA036 OR SAV0381.
OS	Staphylococcus aureus
OS	Staphylococcus aureus (strain N315), and
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;
OC	Bacillus/Staphylococcus group; Staphylococcus.
OX	NCBI_TaxID=1280, 158879, 158878;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus; STRATN=RNA220;
RX	MEDLINE=96004465; PubMed=1151034;
RA	Armstrong-Buisseret L., Cole M.B., Stewart G.S.;
RT	"A homologue to the <i>Escherichia coli</i> alkyl hydroperoxide reductase AhpC is induced by osmotic upshock in <i>Staphylococcus aureus</i> .";
RL	Microbiology 141:1655-1661(1995).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus; STRAIN=RM4220;
RA	Jones E.C., Francis K.P., Stewart G.S.A.B.;
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX	MEDLINE=21311952; PubMed=11418166;
RA	Kuroda M., Ono T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
RA	Cui L., Oguchi A., Aoki T., Nagai Y., Liyan J.-Q., Ito T.,
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA	Mizutani T., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
RA	Sekiimizu K., Hirakawa S., Kubara S., Goto J., Yabuzaki J.,
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA	Hatajiri M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT	"Whole genome sequencing of methicillin-resistant <i>Staphylococcus aureus</i> "; Lancet 357:1225-1240(2001).
RL	CC -1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
CC	DITHIOL FORM (BY SIMILARITY).
CC	-1- INDUCTION: BY OSMOTIC UPSHOCK.
CC	-1- SIMILARITY: BELONGS TO THE AHPC-TSA FAMILY.
DR	EMBL; U92441; AAB51151.1; -
DR	EMBL; AB003330; BAB41533.1; -
DR	EMBL; AP003359; BAB56543.1; -
DR	InterPro; IPR000866; AHPC-TSA.
DR	Pfam; PF00578; AHPC-TSA; 1.
SQ	SEQUENCE 189 AA; 20576 MW; B7134A9C84066B73 CRC64;
Query Match	65.3%; Score 644.5; DB 16; Length 189;
Best Local Similarity	64.2%; Pred. No. 6 6e-52;
Matches	122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;
Qy	1 MSL IN KI KPK KQ AF KG NG - KNG E IE TE K D T G C R W S V F F V P A D F F V C P T E L G D V A D H 59
Db	1 MSL I G E V Q P F R Q A Q F Q S G K D F E V T E A D L K G K S I - V F V P A D F S V C P T E L G D V A D H 59

RL	J. Bacteriol. 179:3944-3949(1997).
DR	EMBL; U94336; AAC45425.1; -.
DR	InterPro; IPR000866; Ahpc-TSA.
DR	Pfam: PF00578; Ahpc-TSA; 1.
SQ	SEQUENCE 187 AA; 20462 MW; 844A58ABC4EGAC4 CRC64;
RESULT	14
Query Match	59.7%; Score 589.5; DB 2; Length 187;
Best Local Similarity	56.9%; Pred. No. 8.1e-47;
Matches	107; Conservative 33; Mismatches 47; Indels 1; Gaps 1;
QY	1 MSLINTKIKPKFKNQAFNGEFTITEKDTEGRMSVFFPYPADTFVCPTELGDVADHYE 60
Db	1 MSLINTKIKPKFKNQAFNGEFTITEKDTEGRMSVFFPYPADTFVCPTELGDVADHYE 60
QY	61 ELQKLGVVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTRNFNDNREDEGLAD 120
Db	60 ELQKLGVVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTRNFNDNREDEGLAD 120
QY	61 AFQKAGAEYIVITDTHFSHKVNRNETSPAVKGKQPLGDPTKLRTRAFGVHTEEGIAL 119
Db	60 AFQKAGAEYIVITDTHFSHKVNRNETSPAVKGKQPLGDPTKLRTRAFGVHTEEGIAL 119
QY	121 RATFVVDPOGIQIAEVTAEGIGRDAASLIRKIKAQAYASHPGVCPAKWKEGATLAP 180
Db	120 RATFVVDPOGIQIAEVTAEGIGRDAASLIRKIKAQAYASHPGVCPAKWKEGATLAP 179
QY	181 SLDLVGKI 188
Db	180 SLDLVGKI 187
RESULT	13
ID	030738 PRELIMINARY; PRT; 187 AA.
AC	030738; DR
DT	01-JAN-1998 (TREMBlrel. 05, Created)
DT	01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE (AHPC).
OS	Treponema pallidum.
OC	Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX	NCBI_TaxID=160;
RP	SEQUENCE FROM N.A.
RC	STRAIN=NICHOSE;
RX	MEDLINE=9833770; PubMed=9665876;
RA	Fraser C.M., Norris S.J., Wainstock G.M., White O., Sutton G.G., Dodson R., Gwynn M., Hickie E.K., Clayton R., Ketchum K.A., Sodergren E., Harcham J.M., McLeod M.P., Salzberg S., Peterson J.T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S., Harsh B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
RA	"Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
RT	Science 281:375-388(1998);
RL	EMBL; AED0122; AAC65497.1; -.
DR	HSSP; P3041; 1PRX.
DR	TIGR; TP0509; -.
DR	InterPro; IPR000866; Ahpc-TSA.
DR	Pfam; PF00578; Ahpc-TSA; 1.
KW	Complete proteome.
SQ	SEQUENCE 188 AA; 20709 MW; 44D2CFDA3420AFE CRC64;
RESULT	15
Query Match	49.5%; Score 488.5; DB 16; Length 188;
Best Local Similarity	49.7%; Pred. No. 1.8e-37;
Matches	93; Conservative 32; Mismatches 61; Indels 1; Gaps 1;
QY	2 SLINTKIKPKFKNQAFNGEFTITEKDTEGRMSVFFPYPADTFVCPTELGDVADHYE 61
Db	3 SLIGKRVIFDKLPAYVGCKFTEVSNASIKGSWAV-FMFYPADTFVCPTELADRVPYS 61
QY	62 LQKLGVVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTRNFNDNREDEGLAD 121
Db	62 FVEIGCKVSVSVDSEYVHKWADATDTPKLYMISDKAGKLAGFFGVLLPDWHALR 121
QY	122 ATFWVVDPOGIQIAEVTAEGIGRDAASLIRKIKAQAYASHPGVCPAKWKEGATLAP 181
Db	122 GTFVVDPOGIQIAEVTAEGIGRDAASLIRKIKAQAYASHPGVCPAKWKEGATLAP 181
QY	182 SLDLVGKI 188
Db	182 IDLIGKI 188
RESULT	15
ID	066779 PRELIMINARY; PRT; 211 AA.
AC	066779; DR
DT	01-AUG-1998 (TREMBlrel. 07, Created)
DT	01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT	01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE	ALKYL HYDROPEROXIDE REDUCTASE.
GN	AHPC OR AQ_486.
OS	Aquifex aeolicus.
OC	Bacteria; Aquificales; Aquificaceae; Aquifex.
OX	NCBI_TaxID=63363;

Query Match 57.1%; Score 563.5; DB 2; Length 187;
 Best Local Similarity 54.3%; Pred. No. 2.1e-44;
 Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSLINTKIKPKFKNQAFNGEFTITEKDTEGRMSVFFPYPADTFVCPTELGDVADHYE 60
 Db 1 MNLINGKLFDFECDAVHDGEETRVSFEDILGKWSI-FFYFADPSFCVCPTELGMDQEHYA 59

QY 61 ELQKLGVVVAVSTDTHTHKAWSSETAKIKYAMIGDPTGALTRNFNDNREDEGLAD 120
 Db 60 HLQELNCVYVSVSDESHVHRAWADATEIGKIKFPLADENGQIARFFGVLDASGMAY 119

QY 121 RATFVVDPOGIQIAEVTAEGIGRDAASLIRKIKAQAYASHPGVCPAKWKEGATLAP 180
 Db 120 RASFIVSPPEGDIKSYEINDMGIGRNAAELVLVKLEASOFVAEHGDVKVCPAWMQPEETIAP 179

[1]
RN SEQUENCE FROM N.A.
RP
RC STRAIN="VF5";
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus."
RL Nature 392:353-358(1998).
DR EMBL: AE000692; AAC06735; 1.
DR HSSP: P30041; 1.PRX
DR InterPro: IPR000866; AhpC-TSA.
DR Pfam: PF00578; AhpC-TSA; 1.
KW Complete proteome:
SEQUENCE 211 AA; 23851 MW; C082545079D87495 CRC64;

Query Match 46.1%; Score 455.5; DB 16; Length 211;
Best Local Similarity 45.0%; Pred. No. 2.5e-34; Matches 85;保守性 41; Mismatches 58; Indels 5; Gaps 3;

Qy :I:KIKPKFKNQAF- KNGEFTIEITEKD--TRGRWSVFFFFPPADFTFVCPTELGDYADHY 59
Db :I:KIKPKFKNQAF- KNGEFTIEITEKD--TRGRWSVFFFFPPADFTFVCPTELGDYADHY 59
18 VQQRKVNFEMETYDPSIGKFGKWWLEDLKERKVVLFEPFPADYFVCPPELADAEKY 76
Qy 60 ERHQKLGDVYAVSTUDTHFKHAWHESSETIAKIKYAMIGSPPTGALTRNFEDNMRDEGLA 119
Db 77 DELKEMGEVISVSTDQKFHVLAWRHDEPLIKNVKYPMGADFTGQVSRLEGWYDENIGLA 136
Qy 120 DRATFWVDPQGIQATEVAGCIGRASDLIRKIKAAQYVASHPGEVCPAKWKEGEATLA 179
Db 137 LRGTFVINPSEGVLVGSEVNFYVNGRNADELVRKMKANVYLMSHPEBACPAKWEPEGKTLK 196
Qy 180 PSDLVGKI 188
Db 197 PSEELVGRV 205

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